FIG. 1

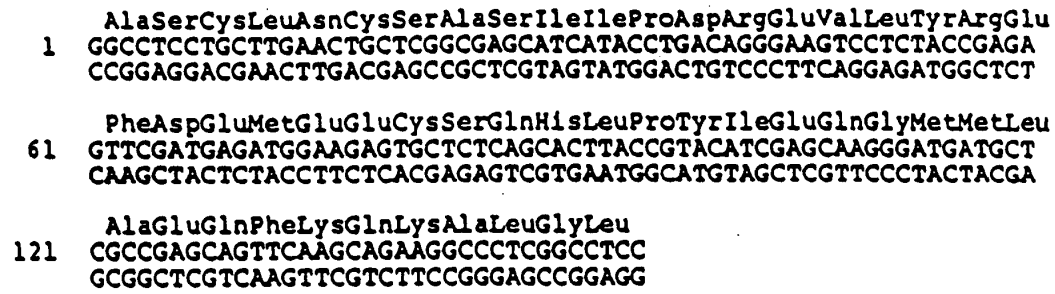

FIG. 3

FIG. 2

```
5-1-1     1                    [ggcctcctgcttgaactgctcggcgagc]ATCATACCTGACAGGGAAG
                                                              ||||||||||||||||||||
81        1                                  GTCCGGGAAGCCGGCAATCATACCTGACAGGGAAG
                                             ||||||||||||||||||||||||||||||||||||
91        1 ctggctgcgtGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAG
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1-2       1           GGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAG

5-1-1    48 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
81       36 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
91       70 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1-2      60 TCCTCTAtCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC

5-1-1   120 TCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCC
            |||||||||||||||||||||||||||||||||
81      108 TCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCC
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
91      142 TCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCC
            |||||||||||||||||||||||||||||||||
1-2     132 TCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCC

81      180 CTGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
91      214 CTGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGA

81      252 TACAATACTTGGCGGGCTTGTCAACGCTGCCTGGtaaccccgccattgcttcattgatggcttttacagctg
            ||||||||||||||||||||||||||||||||||
91      286 TACAATACTTGGCGGGCTTGTCAACGCTGCCTGG

81      324 ctgtcaccagcccactaaccactagccaaa
```

FIG. 4

```
    SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet
  1 GTCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGAT
    CAGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTA

    GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe
 61 GGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTT
    CCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAA

    LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro
121 CAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCC
    GTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGG

    AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe
181 TGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTT
    ACGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAA

    IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla
241 CATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGC
    GTAGTCACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACG

    SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln
301 TTCATTGATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAA
    AAGTAACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTT
```

FIG. 5

```
    AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla
  1 GATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCG
    CTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGC

    TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrp
 61 TACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGG
    ATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACC

    LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu
121 AAGTGTTTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTG
    TTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGAC

    GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys
181 GGCGCTGTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGC
    CCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACG

    MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla
241 ATGTCGGCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCT
    TACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGA

    AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu
301 GCTTTGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTG
    CGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAAC

    ----------Overlap with 81--------------------
    SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArg
361 TCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAG
    AGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTC
```

FIG. 6

```
    AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla
 1  GATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCG
    CTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGC

    TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrp
61  TACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGG
    ATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACC

    LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu
121 AAGTGTTTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTG
    TTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGAC

    GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys
181 GGCGCTGTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGC
    CCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACG

    MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla
241 ATGTCGGCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCT
    TACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGA

    AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu
301 GCTTTGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTG
    CGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAAC

    SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet
361 TCCCGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATG
    AGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTAC

    GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe
421 GAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTC
    CTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAG

    LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro
481 AAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCT
    TTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGA

    AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe
541 GCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTC
    CGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAG

    IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla
601 ATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCT
    TAGTCACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGA

    SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln
661 TCATTGATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAA
    AGTAACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTT
```

FIG. 7

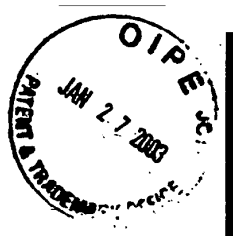

FIG. 8A

```
    SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg
  1 TCCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGG
    AGGTAACTCTGTTAGTGCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCC

    ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly
 61 ACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGC
    TGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCG

    MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu
121 ATGTTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTC
    TACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAG

    ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal
181 ACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTG
    TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCAC
```

FIG. 8B

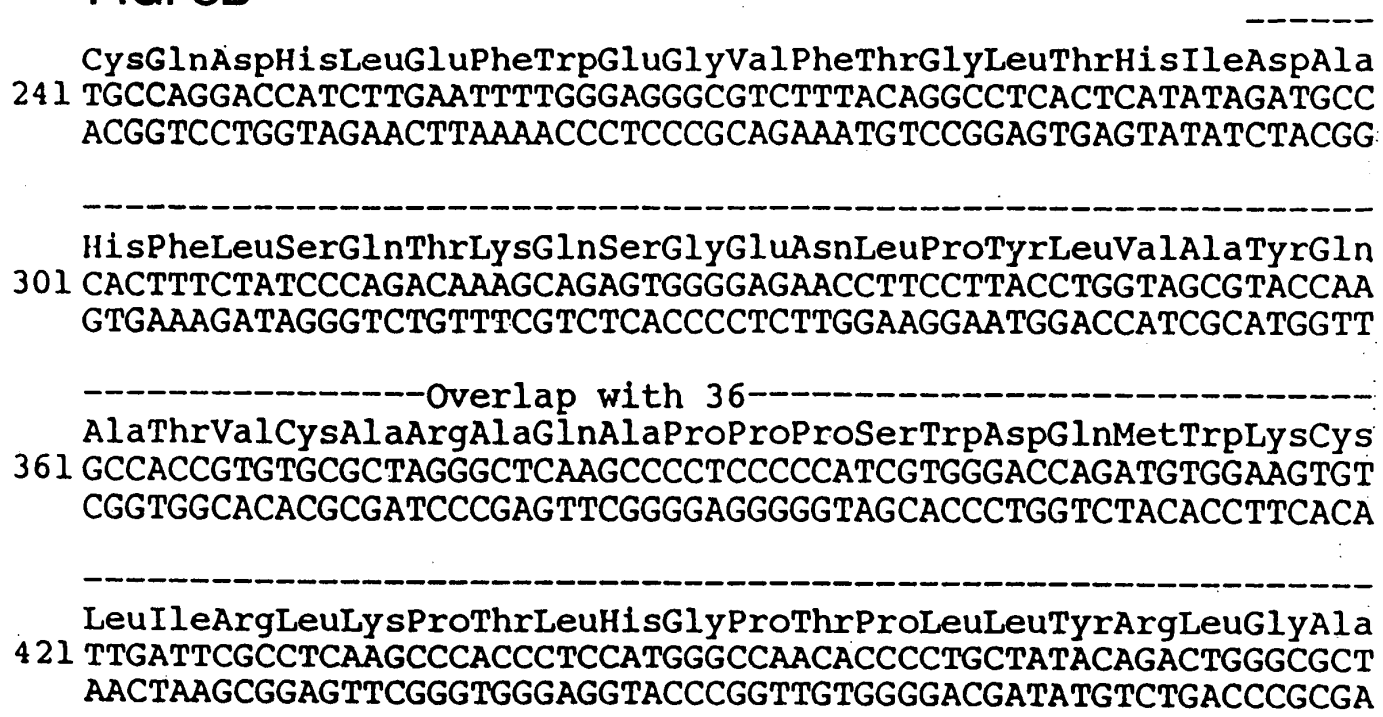

FIG. 9A

```
    SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg
1   TCCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGG
    AGGTAACTCTGTTAGTGCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCC

    ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly
61  ACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGC
    TGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCG

    MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu
121 ATGTTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTC
    TACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAG

    ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal
181 ACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTG
    TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCAC

    CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla
241 TGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCC
    ACGGTCCTGGTAGAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGG

    HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln
301 CACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAA
    GTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTT

    AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys
361 GCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGT
    CGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACA

    LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTryArgLeuGlyAla
421 TTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCT
    AACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGA

    ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer
481 GTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCG
    CAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGC

    AlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeu
541 GCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTG
    CGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAAC

    AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly
601 GCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGG
    CGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCC

    LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu
661 AAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAG
    TTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTC

    CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln
721 TGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAG
    ACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTC

    LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal
781 AAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTC
    TTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAG
```

FIG. 9B

```
    GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer
841 CAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGT
    GTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCA

    GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu
901 GGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTG
    CCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAAC

    MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn
961 ATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAAC
    TACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGACAAGTTG

    IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal
1021 ATATTGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTG
     TATAACCCCCCCACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACAC

    GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp
1081 GGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGAC
     CCGCGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTG

    IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer
1141 ATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGC
     TAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCG

    GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly
1201 GGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGA
     CCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCT

    AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu
1261 GCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAG
     CGGGAGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTC

    GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer
1321 GGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCC
     CCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGG
```

FIG. 10

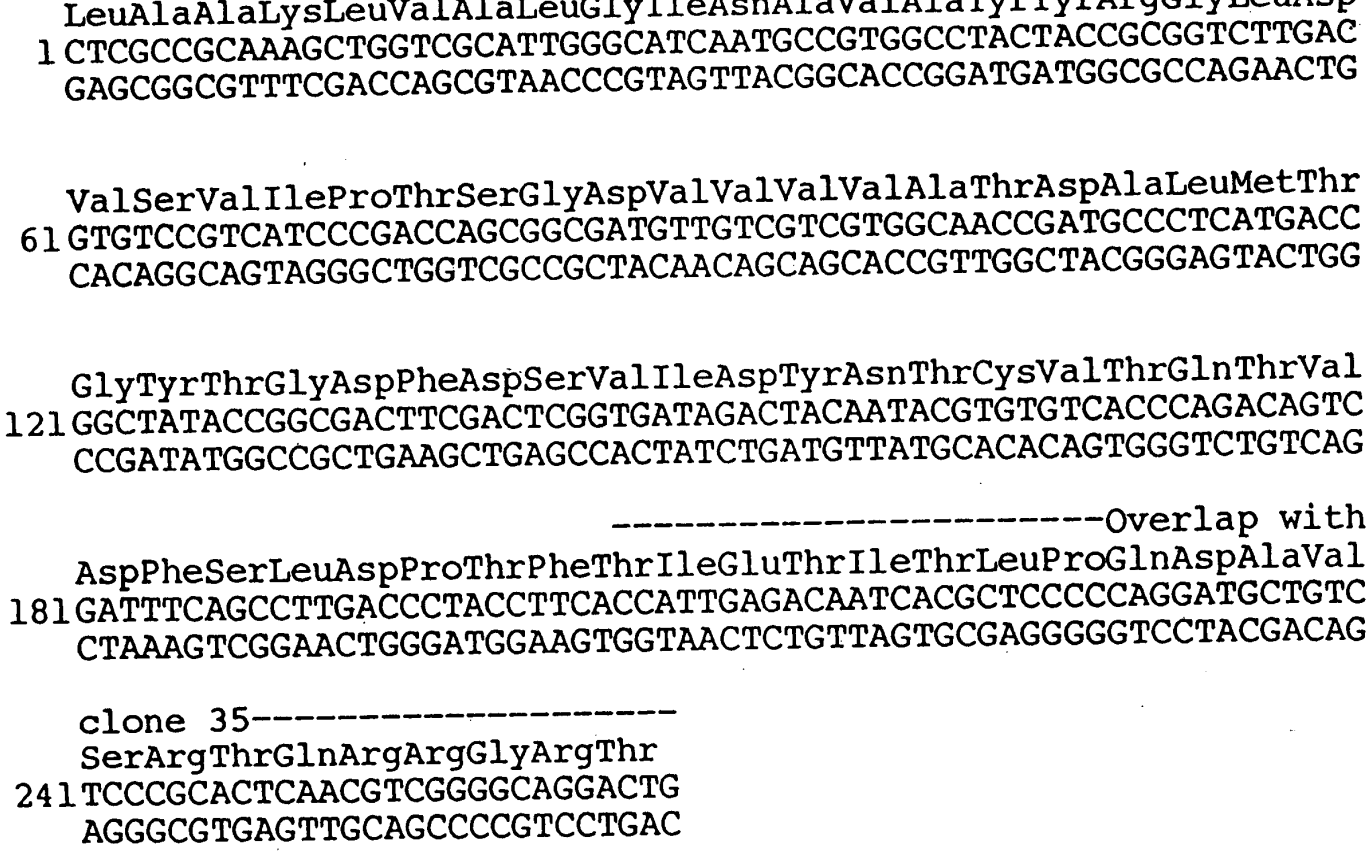

FIG. 11

```
      AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle
   1  GGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAAT
      CCGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTA

      ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys
  61  TACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTG
      ATGGTGACCGTCGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCAC

      SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer
 121  CTCGGGGGGCGCTTATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATC
      GAGCCCCCCGCGAATACTGTATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAG

      IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal
 181  CATCTTGGGCATCGGCACTGTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGT
      GTAGAACCCGTAGCCGTGACAGGAACTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACA

      LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal
 241  GCTCGCCACCGCCACCCCTCCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGGAGGT
      CGAGCGGTGGCGGTGGGGAGGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCA

      AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle
 301  TGCTCTGTCCACCACCGGAGAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAAT
      ACGAGACAGGTGGTGGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTA
                                                    --------

      LysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAla
 361  CAAGGGGGGGAGACATCTCATCTTCTGTCATTCAAAGAAGAAGTGCGACGAACTCGCCGC
      GTTCCCCCCCCTCTGTAGAGTAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCG
      ----------------------Overlap with 37b---------------------

      LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal
 421  AAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGT
      TTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCA
      ----------
      IleProThr
 481  CATCCCGACCAG
      GTAGGGCTGGTC
```

FIG. 12

FIG. 13

```
    ------------------------------------------------------------
      CysSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCys
  1 ACTGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGT
    TGACGTCGGAGTGACATTGGGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCA

    ------------------------------------------------------------
      ThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeu
 61 GTACCACTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGT
    CATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACA.

    ---------------Overlap with 33b-----------------------------
      SerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPhe
121 TGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCT
    ACTCGCTGAAATTCTGGACCGATTTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGA

    ----------------------------------------
      ValSerCysGlnArgGlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArg
181 TTGTGTCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTC
    AACACAGGACGGTCGCGCCCATATTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAG

      CysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGly
241 GCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCG
    CGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGC

      ProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGly
301 GTCCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGG
    CAGGATCCTGGACGTCCTTGTACACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCC

      ProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGlu
361 GCCCCTGTACCCCCCTTCCTGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAG
    CGGGGACATGGGGGGAAGGACGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTC

      GluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAsp
421 AGGAATATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTG
    TCCTTATACACCTCTATTCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGAC

      AsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu
481 ACAATCTCAAATGCCCGTGCCAGGTCCCATCGCCCGAATTTTTCACAGAAT
    TGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTA
```

FIG. 14A

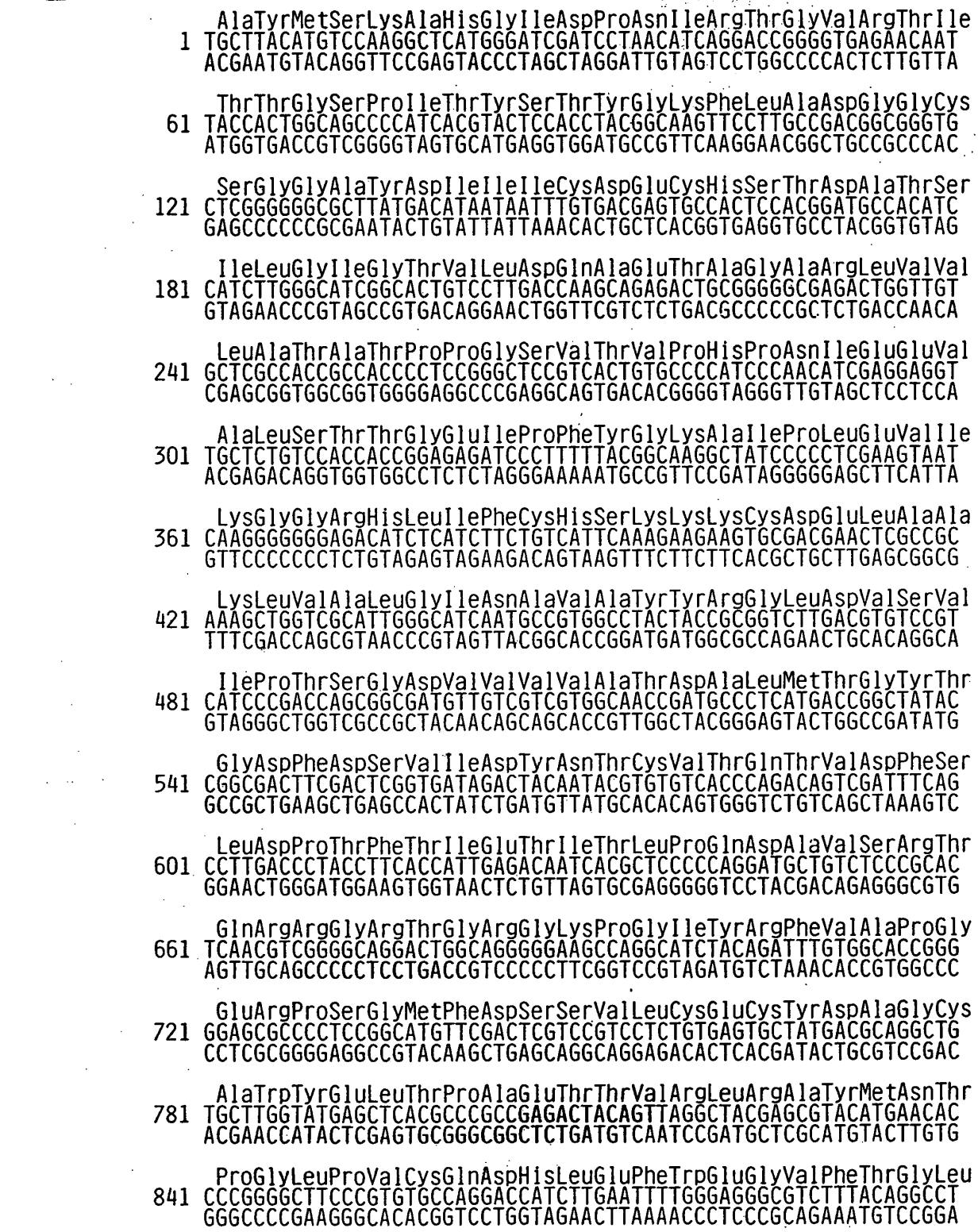

FIG. 14B

```
      ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAspLeuProTyr
901   CACTCATATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTA
      GTGAGTATATCTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAAT

      LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAsp
961   CCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGA
      GGACCATCGCATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCT

      GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu
1021  CCAGATGTGGAAGTGTTTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCT
      GGTCTACACCTTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGA

      TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle
1081  ATACAGACTGGGCGCTGTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACAT
      TATGTCTGACCCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTA

      MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly
1141  CATGACATGCATGTCGGCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGG
      GTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCC

      ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg
1201  CGTCCTGGCTGCTTTGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAG
      GCAGGACCGACGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTC

      ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe
1261  GGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTT
      CCAGCAGAACAGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAA

      AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla
1321  CGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGC
      GCTACTCTACCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCG

      GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal
1381  CGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGT
      GCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCA

      IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet
1441  TATCGCCCCTGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATAT
      ATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATA

      TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro
1501  GTGGAACTTCATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCC
      CACCTTGAAGTAGTCACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGG

      AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln
1561  CGCCATTGCTTCATTGATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCA
      GCGGTAACGAAGTAACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGT

      ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla
1621  AACCCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGC
      TTGGGAGGAGAAGTTGTATAACCCCCCCACCCACCGACGGGTCGAGCGGCGGGGGCCACG

      AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly
1681  CGCTACTGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGG
      GCGATGACGGAAACACCCGCGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACCC
```

FIG. 14C

```
      LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla
1741  GAAGGTCCTCATAGACATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGC
      CTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCG

      PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla
1801  ATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGC
      TAAGTTCTAGTACTCGCCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCG

      IleLeuSerProGlyAlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHis
1861  CATCCTCTCGCCCGGAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCA
      GTAGGAGAGCGGGCCTCGGGAGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGT

      ValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArg
1921  CGTTGGCCCGGGCGAGGGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCG
      GCAACCGGGCCCGCTCCCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGC

      GlyAsnHisValSerProThrHisTyrValProGluSerAspAlaAlaAlaArgValThr
1981  GGGGAACCATGTTTCCCCCACGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCAC
      CCCCTTGGTACAAAGGGGGTGCGTGATGCACGGCCTCTCGCTACGTCGACGGGCGCAGTG

      AlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSer
2041  TGCCATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAG
      ACGGTATGAGTCGTCGGAGTGACATTGGGTCGAGGACTCCGCTGACGTGGTCACCTATTC

      SerGluCysThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCys
2101  CTCGGAGTGTACCACTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATG *
      GAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATAC

      GluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGly
2161  CGAGGTGTTGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTGG
      GCTCCACAACTCGCTGAAATTCTGGACCGATTTTCGATTCGAGTACGGTGTCGACGGACC

      IleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMet
2221  GATCCCCTTTGTGTCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCAT
      CTAGGGGAAACACAGGACGGTCGCGCCCATATTCCCCCAGACCGCTCACCTGCCGTAGTA

      HisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArg
2281  GCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAG
      CGTGTGAGCGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTC

      IleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyr
2341  GATCGTCGGTCCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCTA
      CTAGCAGCCAGGATCCTGGACGTCCTTGTACACCTCACCCTGGAAGGGGTAATTACGGAT

      ThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgVal
2401  CACCACGGGCCCCTGTACCCCCCTTCCTGCGCCGAACTACACGTTCGCGCTATGGAGGGT
      GTGGTGCCCGGGGACATGGGGGGAAGGACGCGGCTTGATGTGCAAGCGCGATACCTCCCA

      SerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMet
2461  GTCTGCAGAGGAATATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTAT
      CAGACGTCTCCTTATACACCTCTATTCCGTCCACCCCCTGAAGGTGATGCACTGCCCATA

      ThrThrAspAsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu
2521  GACTACTGACAATCTCAAATGCCCGTGCCAGGTCCCATCGCCCGAATTTTTCACAGAAT
      CTGATGACTGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTA
```

FIG. 15

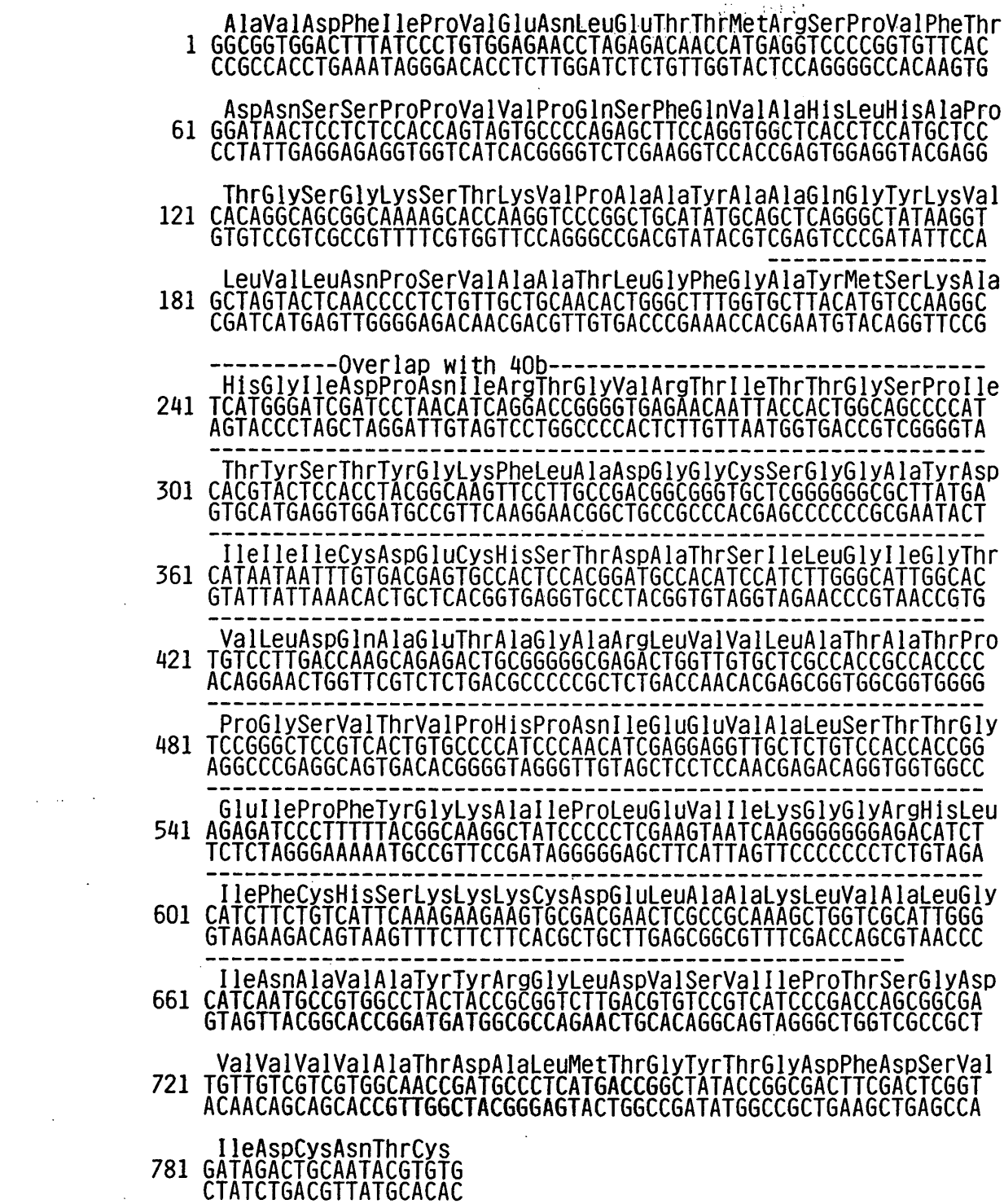

FIG. 16

FIG. 17

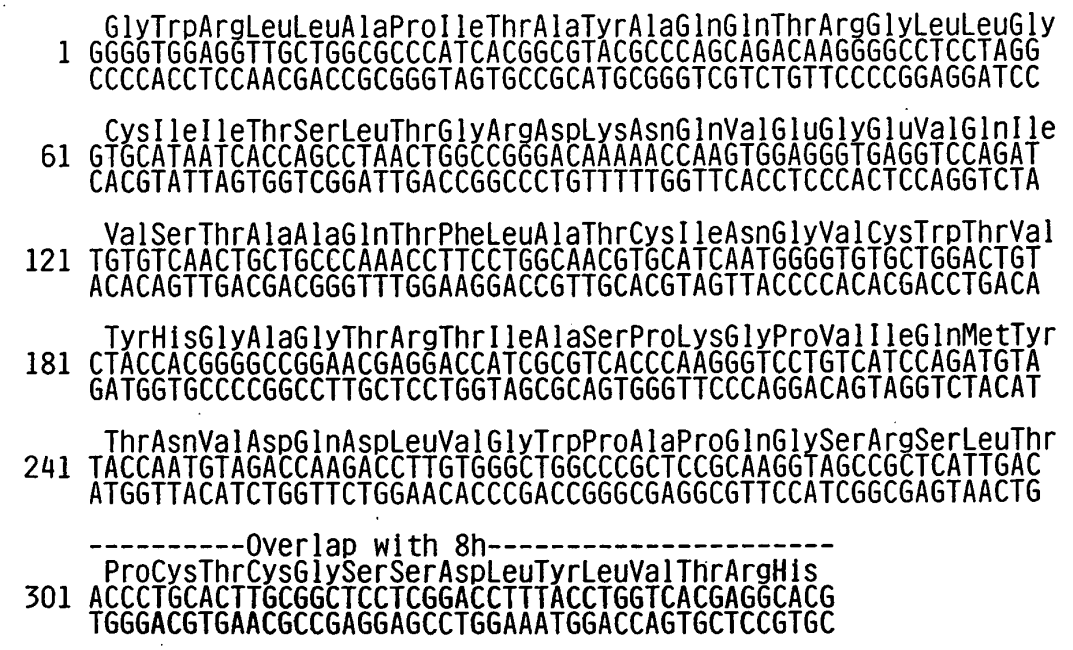

FIG. 18

FIG. 19

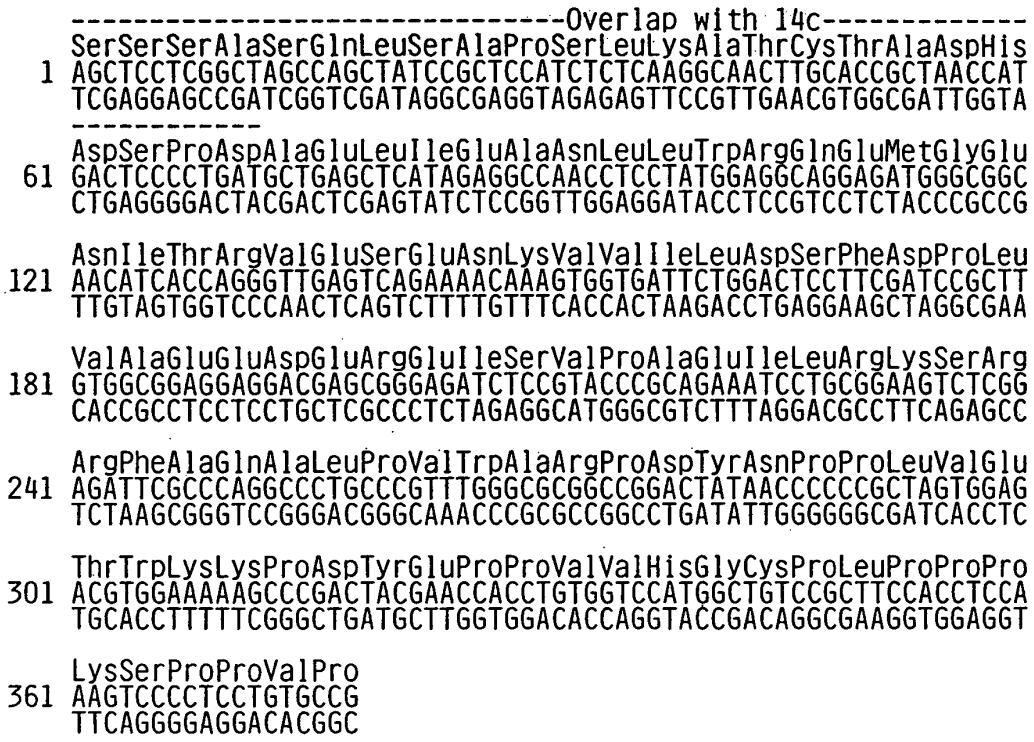

FIG. 20

FIG. 21

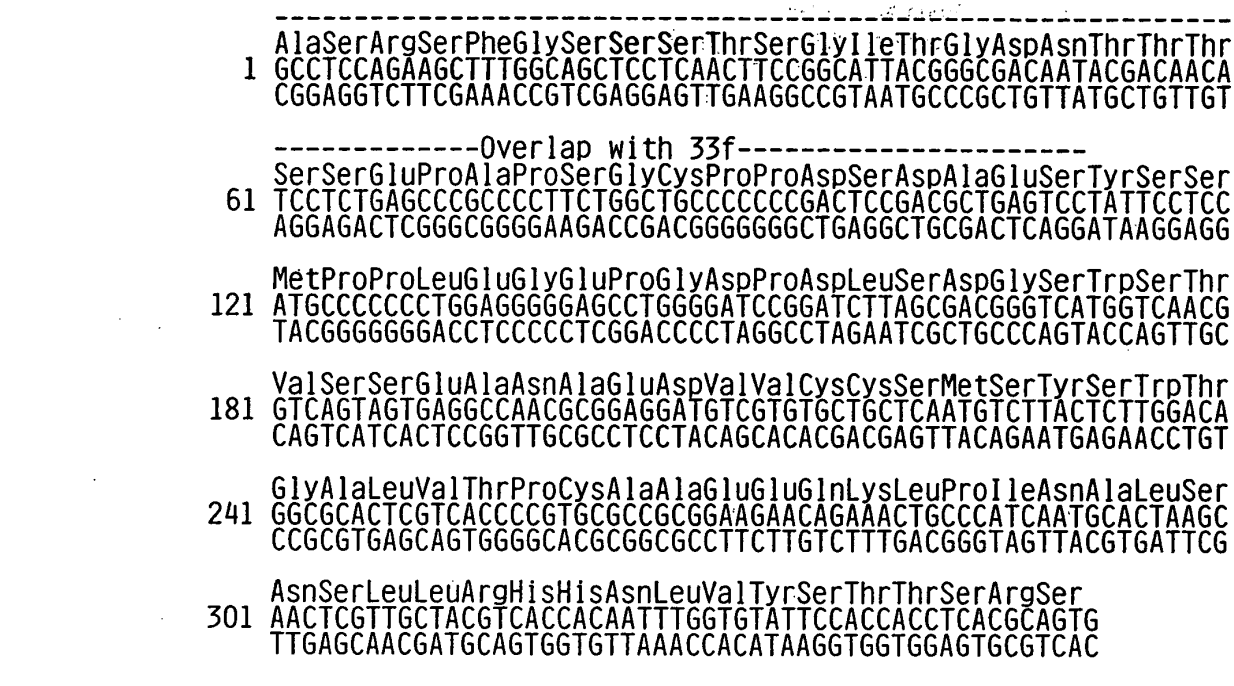

FIG. 22

FIG. 23

```
    GlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyr
1   GGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATATTACAAGCGCTAT
    CCGCCACAACAAGAGCAGCCCAACTACCGCGACTGAGACAGTGGTATAATGTTCGCGATA

    IleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHis
61  ATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGAAGCGCAACTGCAC
    TAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTG

    ValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeuMetCys
121 GTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCATCTTACTCATGTGT
    CACACCTAAGGGGGGGAGTTGCAGGCTCCCCCCGCGCTGCGGCAGTAGAATGAGTACACA

    AlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPheGlyPro
181 GCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCCGTCTTCGGACCC
    CGACATGTGGGCTGAGACCATAAACTGTAGTGGTTTAACGACGACCGGCAGAAGCCTGGG

    LeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGlnGlyLeu
241 CTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGCGTCCAAGGCCTT
    GAAACCTAAGAAGTTCGGTCAAACGAATTTCATGGGATGAAACACGCGCAGGTTCCGGAA

     euArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMetValIle
301 CTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATC
    GAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAG

                                 ----------------------------------------
    IleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeuArgAsp
361 ATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGAC
    TAATTCAATCCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTGAGGAGAAGCCCTG

    --------------------Overlap with 7f -----------------------
    TrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPheSerGln
421 TGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTTCTCCCAA
    ACCCGCGTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAGCAGAAGAGGGTT

    ------------------------------
    MetGluThrLysLeuIleThrTrpGly
481 ATGGAGACCAAGCTCATCACGTGGGGGGC
    TACCTCTGGTTCGAGTAGTGCACCCCCCG
```

FIG. 24

FIG. 25

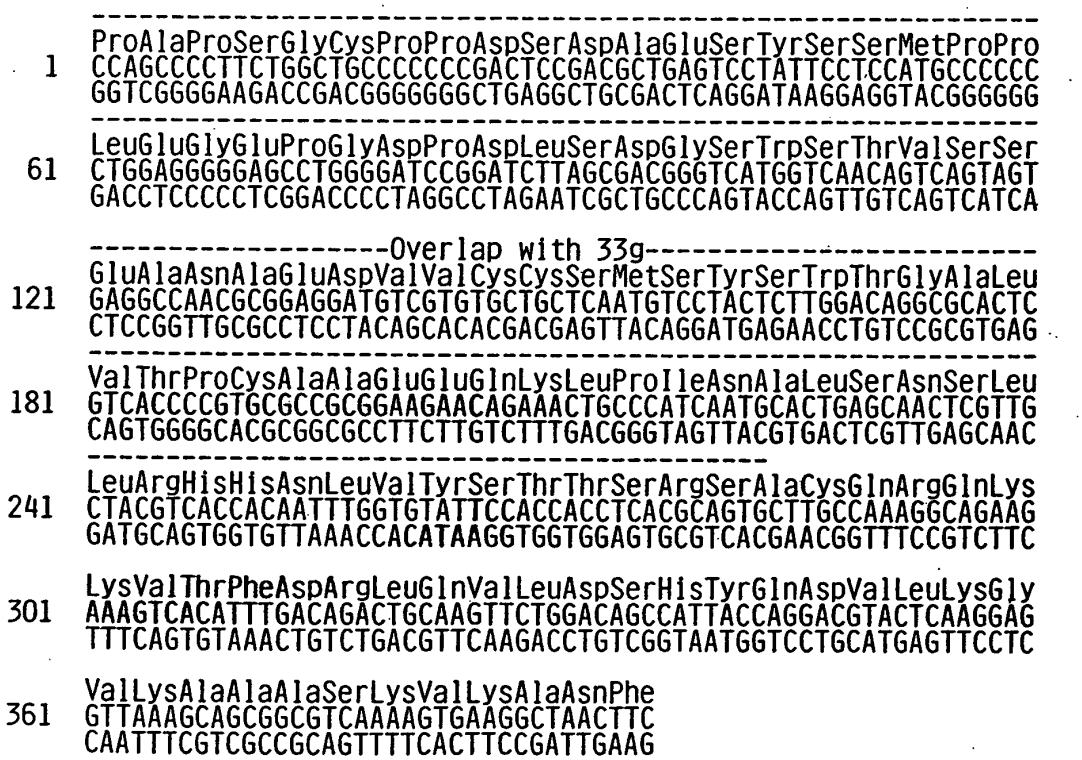

FIG. 26A

```
  GluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrp
1 GGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTGCAGACGCGCGCGTCTGCTCCTGCTTGT
  CCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGACGAACA

  MetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAla
61 GGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTTAATG
  CCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCTTGGAGCATTATGAATTAC

  AlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrp
121 CAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCGTGTTCTTCTGCTTTGCAT
  GTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAAACGTA

  TyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeu
181 GGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTGGCCTC
  CCATAAACTTCCCATTCACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACCGGAG

  LeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAla
241 TCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGTGGCCG
  AGGAGGACGAGGACAACCGCAACGGGGTCGCCCGCATGCGCGACCTGTGCCTCCACCGGC

  SerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLys
301 CGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATATTACA
  GCAGCACACCGCCACAACAAGAGCAGCCCAACTACCGCGACTGAGACAGTGGTATAATGT

  ArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGln
361 AGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGAAGCGC
  TCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTTCGCG

  LeuHisValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeu
421 AACTGCACGTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCATCTTAC
  TTGACGTGCACACCTAAGGGGGGGAGTTGCAGGCTCCCCCCGCGCTGCGGCAGTAGAATG

  MetCysAlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPhe
481 TCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCCGTCT
  AGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGTTTAACGACGACCGGCAGA

  GlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGln
541 TCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGCGTCC
  AGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTCATGGGATGAAACACGCGCAGG

  GlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMet
601 AAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAA
  TTCCGGAAGAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTT

  ValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeu
661 TGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTC
  ACCAGTAGTAATTCAATCCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTGAGGAG

  ArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPhe
721 TTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCT
  AAGCCCTGACCCGCGTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAGCAGA

  SerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGlyAspIle
781 TCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGGTGACA
  AGAGGGTTTACCTCTGGTTCGAGTAGTGCACCCCCCGTCTATGGCGGCGCACGCCACTGT

  IleAsnGlyLeuProValSerAlaArgArgGlyArgGluIleLeuLeuGlyProAlaAsp
841 TCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCCAGCCG
  AGTAGTTGCCGAACGGACAAAGGCGGGCGTCCCCGGCCCTCTATGACGAGCCCGGTCGGC

  GlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThr
901 ATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCAGCAGA
  TACCTTACCAGAGGTTCCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGTCGTCT
```

FIG. 26B

```
                ArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGlu
961  CAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCAAGTGG
     GTTCCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTTGGTTCACC

                GlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGly
1021 AGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCATCAATG
     TCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAGGACCGTTGCACGTAGTTAC

                ValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyPro
1081 GGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAAGGGTC
     CCCACACGACCTGACAGATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGGTTCCCAG

                ValIleGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGly
1141 CTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAG
     GACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGCGTTC

                SerArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHis
1201 GTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACGAGGC
     CATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCAGTGCTCCG

                AlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArg
1261 ACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTCGCCCC
     TGCGGCTACAGTAAGGGCACGCGGCCGCCCCACTATCGTCCCCGTCGGACGACAGCGGGG

                ProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAla
1321 GGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGGGCACG
     CCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCCAGGCGACAACACGGGGCGCCCCGTGC

                ValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIle
1381 CCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGACTTTA
     GGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTCACCGATTCCGCCACCTGAAAT

                ProValGluAsnLeuGluThrThrMetArgSerProValPheThrAspAsnSerSerPro
1441 TCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTCCTCTC
     AGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAGGAGAG

                ProValValProGlnSerPheGlnValAlaHisLeuHisAlaProThrGlySerGlyLys
1501 CACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAGCGGCA
     GTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTCGCCGT

                SerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsnPro
1561 AAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAACC
     TTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTGG

                SerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAspPro
1621 CCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGATC
     GGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTAG

                AsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThrTyr
1681 CTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACCT
     GATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGGA

                GlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCysAsp
1741 ACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGTG
     TGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACAC

                GluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlnAla
1801 ACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGACCAAG
     TGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACTGGTTC

                GluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerValThr
1861 CAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTCA
     GTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAGT

                ValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPheTyr
1921 CTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTTT
     GACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAAA
```

FIG. 26C

```
                GlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHisSer
1981 ACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCATT
     TGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTAA

                LysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAla
2041 CAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTGG
     GTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCACC

                TyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValValAla
2101 CCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTGG
     GGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCACC

                ThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThr
2161 CAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAATA
     GTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTAT

                CysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThr
2221 CGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATCA
     GCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAGT

                LeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysPro
2281 CGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAGC
     GCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTCG

                GlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSerVal
2341 CAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCCG
     GTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGC

                LeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThrThr
2401 TCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACTA
     AGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGAT

                ValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeuGlu
2461 CAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTTG
     GTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAAC

                PheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGlnThr
2521 AATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAGA
     TTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTCT

                LysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAlaArg
2581 CAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTA
     GTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGAT

                AlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLysPro
2641 GGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAGC
     CCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTCG

                ThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIleThr
2701 CCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATCA
     GGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAGT

                LeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluValVal
2761 CCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTCG
     GGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAGC

                ThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuSer
2821 TCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTGT
     AGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGACA

                ThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIlePro
2881 CAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATAC
     GTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTATG
```

FIG. 26D

```
                TyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeu
3001 CGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCC
     GCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGG

                GlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLys
3061 TGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAAA
     ACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTTT

                LeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAla
3121 AACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTGG
     TTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAACC

                GlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAla
3181 CGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCTG
     GCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGAC

                ValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrpVal
3241 CTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGGG
     GACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACCC

                AlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGly
3301 TGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCTG
     ACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGAC

                AlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGly
3361 GCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTATG
     CGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATAC

                AlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerThr
3421 GCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCCA
     CGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGGT

                GluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyVal
3481 CGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCG
     GCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCGC

                ValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrpMet
3541 TGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGGA
     ACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACCT

                AsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrValPro
3601 TGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTGC
     ACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCACG

                GluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGlnLeu
3661 CGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAGC
     GCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTCG

                LeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySerTrp
3721 TCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCCT
     AGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGGA

                LeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeuLys
3781 GGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTAA
     CCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGATT

                AlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyrLys
3841 AAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTATA
     TTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATAT

                GlyValTrpArgValAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIleThr
3901 AGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATCA
     TCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAGT
```

FIG. 26E

```
                SerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAlaPro
4021 GGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCGC
     CCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGCG

                AsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGlnVal
4081 CGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAGGCAGG
     GCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATACACCTCTATTCCGTCC

                GlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnVal
4141 TGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTGCCAGG
     ACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAGTTTACGGGCACGGTCC

                ProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProPro
4201 TCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCCC
     AGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGGG

                CysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProVal
4261 CCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCGG
     GGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGCC

                GlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeuThr
4321 TAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTCA
     ATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAGT

                AspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProPro
4381 CTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCCC
     GACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGGG

                SerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThr
4441 CCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGCA
     GGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACGT

                AlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGlu
4501 CCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAGG
     GGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTCC

                MetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSerPhe
4561 AGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCCT
     TCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGGA

                AspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArg
4621 TCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTGC
     AGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGACG

                LysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProPro
4681 GGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCCC
     CCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGGG

                LeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysProLeu
4741 CGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGTCCGC
     GCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACAGGCG

                ProProProLysSerProProValProProProArgLysLysArgThrValValLeuThr
4801 TTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTCA
     AAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAGT

                GluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerSer
4861 CTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCCT
     GACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGGA

                ThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyCys
4921 CAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGCT
     GTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCGA

                ProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProGly
4981 GCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCTG
     CGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGAC
```

FIG. 26F

```
      AspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGluAsp
5041  GGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAGG
      CCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTCC

      ValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAlaAla
5101  ATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCCG
      TACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGGC

      GluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsnLeu
5161  CGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAATT
      GCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTAA

      ValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAspArg
5221  TGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGACA
      ACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTGT

      LeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAlaSer
5281  GACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCGT
      CTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGCA

      LysValLysAlaAsnLeu
5341  CAAAAGTGAAGGCTAACTTG
      GTTTTCACTTCCGATTGAAC
```

FIG. 30

```
      ------------------------------------------------------------
      GlyGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCys
1     GGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCAAGCGGCGTACTGACAACTAGCTGT
      CCCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGTTCGCCGCATGACTGTTGATCGACA
      ------------------------------------------------------------
      GlyAsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGln
61    GGTAACACCCTCACTTGTTACATCAAGGCCCGAGCAGCCTGTCGAGCCGCAGGGCTCCAG
      CCATTGTGGGAGTGAACAATGTAGTTCCGGGCTCGTCGGACAGCTCGGCGTCCCGAGGTC

      ------------Overlap with 19g-------------------------------
      AspCysThrMetLeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyVal
121   GACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTC
      CTGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAG
      ----------------
      GlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaPro
181   CAGGAGGACGCGGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCC
      GTCCTCCTGCGCCGCTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGG

      ProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsn
241   CCTGGGGACCCCCCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAAC
      GGACCCCTGGGGGGTGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTG

      ValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThr
301   GTGTCAGTCGCCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACA
      CACAGTCAGCGGGTGCTGCCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGT

      ThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeu
361   ACCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTA
      TGGGGGGAGCGCTCTCGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGAT

      GlyAsnIleIleMetPheAlaProThrLeuTrpAla
421   GGCAACATAATCATGTTTGCCCCCACACTGTGGGCG
      CCGTTGTATTAGTACAAACGGGGGTGTGACACCCGC
```

FIG. 27

FIG. 28

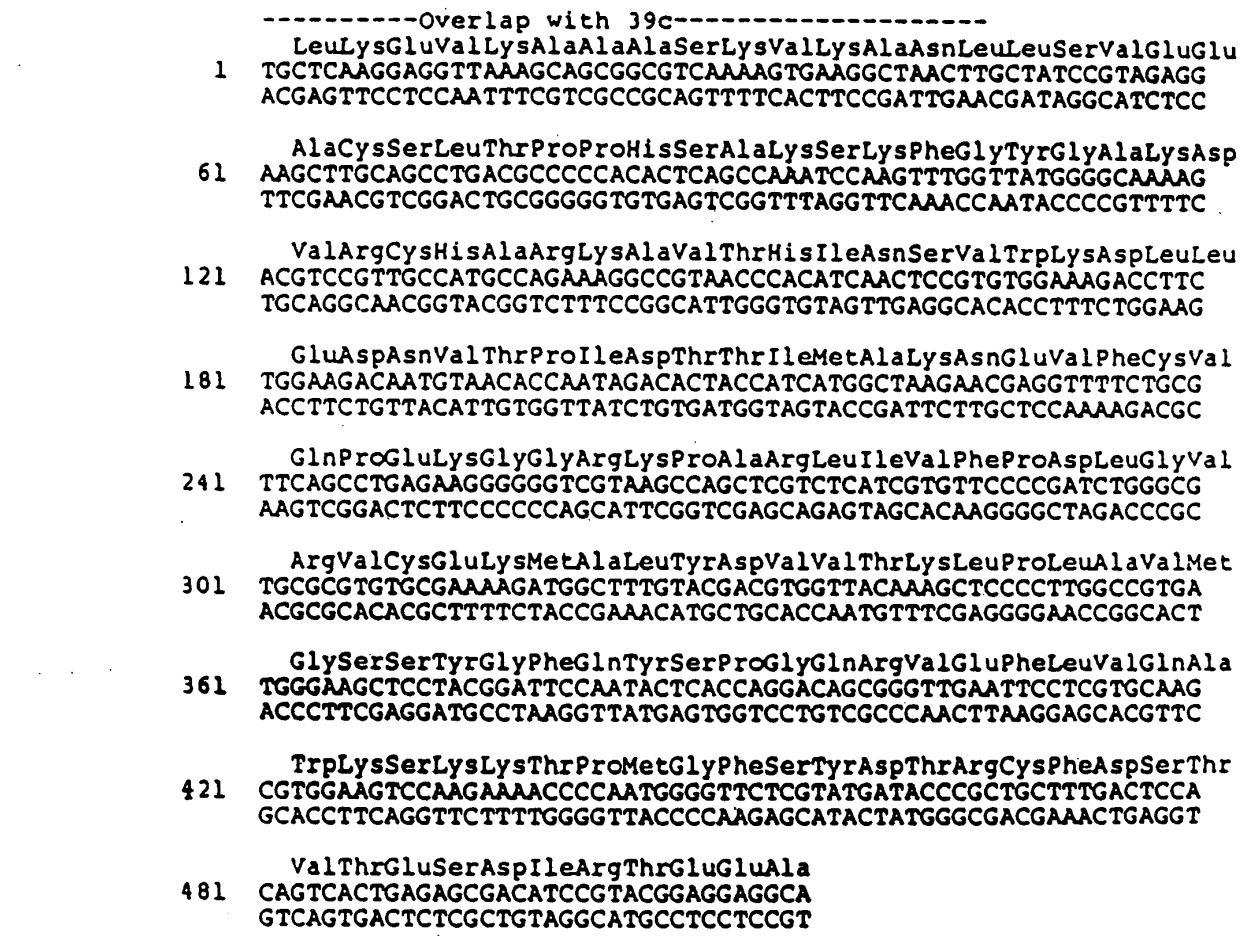

FIG. 29

```
    ------------------------------------------------------------
    GluPheLeuValGlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAspThr
  1 GAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGATACC
    CTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTACCCCAAGAGCATACTATGC

    -------------Overlap with 35f----------------------
    ArgCysPheAspSerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGln
 61 CGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAA
    GCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTT

    CysCysAspLeuAspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeuTyr
121 TGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCCCTCACCGAGAGGCTTTAT
    ACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGGGAGTGGCTCTCCGAAATA

    ValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAla
181 GTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCG
    CAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGC

    SerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAla
241 AGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGGGCA
    TCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACGATGTAGTTCCGGGCCCGT

    AlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuVal
301 GCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCGACGACTTAGTC
    CGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCACACACCGCTGCTGAATCAG

    ValIleCysGluSerAlaGlyValGlnGluAspAlaAla
361 GTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAG
    CAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTC
```

FIG. 31

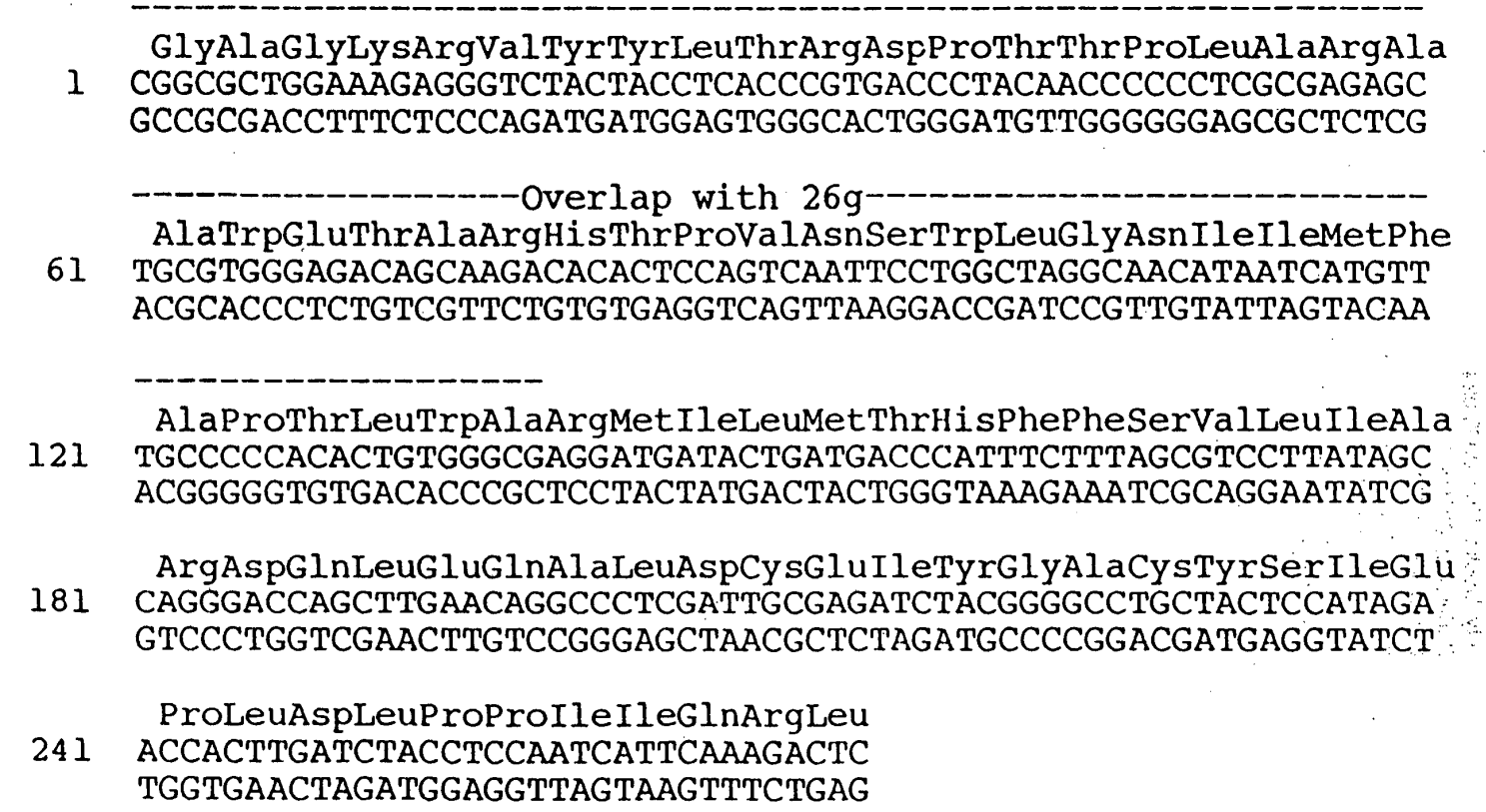

FIG. 32A

```
      IlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsn
    1 CCATATTTAAAATCAGGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCCTGCA
      GGTATAAATTTTAGTCCTACATGCACCCTCCCCAGCTTGTGTCCGACCTTCGACGGACGT

      TrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeu
   61 ACTGGACGCGGGGCGAACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGT
      TGACCTGCGCCCCGCTTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCA

      LeuLeuThrThrThrGlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeu
  121 TACTGCTGACCACTACACAGTGGCAGGTCCTCCCGTGTTCCTTCACAACCCTACCAGCCT
      ATGACGACTGGTGATGTGTCACCGTCCAGGAGGGCACAAGGAAGTGTTGGGATGGTCGGA

      SerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyVal
  181 TGTCCACCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGG
      ACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAACACCTGCACGTCATGAACATGCCCC

      GlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeu
  241 TGGGGTCAAGCATCGCGTCCTGGGCCATTAAGTGGGAGTACGTCGTTCTCCTGTTCCTTC
      ACCCCAGTTCGTAGCGCAGGACCCGGTAATTCACCCTCATGCAGCAAGAGGACAAGGAAG

      LeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGlu
  301 TGCTTGCAGACGCGCGCGTCTGCTCCTGCTTGTGGATGATGCTACTCATATCCCAAGCGG
      ACGAACGTCTGCGCGCGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCC

      AlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeu
  361 AGGCGGCTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTC
      TCCGCCGAAACCTCTTGGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCCAG

      ValSerPheLeuValPhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGly
  421 TTGTATCCTTCCTCGTGTTCTTCTGCTTTGCATGGTATTTGAAGGGTAAGTGGGTGCCCG
      AACATAGGAAGGAGCACAAGAAGACGAAACGTACCATAAACTTCCCATTCACCCACGGGC

      AlaValTyrThrPheTyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGln
  481 GAGCGGTCTACACCTTCTACGGGATGTGGCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCC
      CTCGCCAGATGTGGAAGATGCCCTACACCGGAGAGGAGGACGAGGACAACCGCAACGGGG

      ArgAlaTyrAlaLeuAspThrGluValAlaAlaSerCysGlyGlyValValLeuValGly
  541 AGCGGGCGTACGCGCTGGACACGGAGGTGGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCG
      TCGCCCGCATGCGCGACCTGTGCCTCCACCGGCGCAGCACACCGCCACAACAAGAGCAGC

      LeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrp
  601 GGTTGATGGCGCTGACTCTGTCACCATATTACAAGCGCTATATCAGCTGGTGCTTGTGGT
      CCAACTACCGCGACTGAGACAGTGGTATAATGTTCGCGATATAGTCGACCACGAACACCA

      LeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsn
  661 GGCTTCAGTATTTTCTGACCAGAGTGGAAGCGCAACTGCACGTGTGGATTCCCCCCCTCA
      CCGAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTGCACACCTAAGGGGGGGAGT

      ValArgGlyGlyArgAspAlaValIleLeuLeuMetCysAlaValHisProThrLeuVal
  721 ACGTCCGAGGGGGGCGCGACGCCGTCATCTTACTCATGTGTGCTGTACACCCGACTCTGG
      TGCAGGCTCCCCCCGCGCTGCGGCAGTAGAATGAGTACACACGACATGTGGGCTGAGACC

      PheAspIleThrLysLeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSer
  781 TATTTGACATCACCAAATTGCTGCTGGCCGTCTTCGGACCCCTTTGGATTCTTCAAGCCA
      ATAAACTGTAGTGGTTTAACGACGACCGGCAGAAGCCTGGGGAAACCTAAGAAGTTCGGT

      LeuLeuLysValProTyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAla
  841 GTTTGCTTAAAGTACCCTACTTTGTGCGCGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAG
      CAAACGAATTTCATGGGATGAAACACGCGCAGGTTCCGGAAGAGGCCAAGACGCGCAATC
```

FIG. 32B

```
      ArgLysMetIleGlyGlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThr
901   CGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATCATTAAGTTAGGGGCGCTTA
      GCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAGTAATTCAATCCCCGCGAAT

      GlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArg
961   CTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGACTGGGCGCACAACGGCTTGC
      GACCGTGGATACAAATATTGGTAGAGTGAGGAGAAGCCCTGACCCGCGTGTTGCCGAACG

      AspLeuAlaValAlaValGluProValValPheSerGlnMetGluThrLysLeuIleThr
1021  GAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTTCTCCCAAATGGAGACCAAGCTCATCA
      CTCTAGACCGGCACCGACATCTCGGTCAGCAGAAGAGGGTTTACCTCTGGTTCGAGTAGT

      TrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArg
1081  CGTGGGGGGCAGATACCGCCGCGTGCGGTGACATCATCAACGGCTTGCCTGTTTCCGCCC
      GCACCCCCCGTCTATGGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGGCGGG

      ArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeu
1141  GCAGGGGCCGGGAGATACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGGTGGAGGT
      CGTCCCCGGCCCTCTATGACGAGCCCGGTCGGCTACCTTACCAGAGGTTCCCCACCTCCA

      LeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThr
1201  TGCTGGCGCCCATCACGGCGTACGCCCAGCAGACAAGGGGCCTCCTAGGGTGCATAATCA
      ACGACCGCGGGTAGTGCCGCATGCGGGTCGTCTGTTCCCCGGAGGATCCCACGTATTAGT

      SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla
1261  CCAGCCTAACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTG
      GGTCGGATTGACCGGCCCTGTTTTTGGTTCACCTCCCACTCCAGGTCTAACACAGTTGAC

      AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAla
1321  CTGCCCAAACCTTCCTGGCAACGTGCATCAATGGGGTGTGCTGGACTGTCTACCACGGGG
      GACGGGTTTGGAAGGACCGTTGCACGTAGTTACCCCACACGACCTGACAGATGGTGCCCC

      GlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyrThrAsnValAsp
1381  CCGGAACGAGGACCATCGCGTCACCCAAGGGTCCTGTCATCCAGATGTATACCAATGTAG
      GGCCTTGCTCCTGGTAGCGCAGTGGGTTCCCAGGACAGTAGGTCTACATATGGTTACATC

      GlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThrProCyrThrCys
1441  ACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAGGTAGCCGCTCATTGACACCCTGCACTT
      TGGTTCTGGAACACCCGACCGGGCGAGGCGTTCCATCGGCGAGTAACTGTGGGACGTGAA

      GlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIleProValArgArgArg
1501  GCGGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTCCCGTGCGCCGGC
      CGCCGAGGAGCCTGGAAATGGACCAGTGCTCCGTGCGGCTACAGTAAGGGCACGCGGCCG

      GlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSer
1561  GGGGTGATAGCAGGGGCAGCCTGCTGTCGCCCCGGCCCATTTCCTACTTGAAAGGCTCCT
      CCCCACTATCGTCCCCGTCGGACGACAGCTGGGCCGGGTAAAGGATGAACTTTCCGAGGA

      GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys
1621  CGGGGGGTCCGCTGTTGTGCCCCGCGGGGCACGCCGTGGGCATATTTAGGGCCGCGGTGT
      GCCCCCCAGGCGACAACACGGGGCGCCCCGTGCGGCACCCGTATAAATCCCGGCGCCACA

      ThrArgGlyValAlaLysAlaValAspPheIleProValGluAsnLeuGluThrThrMet
1681  GCACCCGTGGAGTGGCTAAGGCGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAACCA
      CGTGGGCACCTCACCGATTCCGCCACCTGAAATAGGGACACCTCTTGGATCTCTGTTGGT
```

FIG. 32C

```
      ArgSerProValPheThrAspAsnSerSerProProValValProGlnSerPheGlnVal
1741  TGAGGTCCCCGGTGTTCACGGATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTCCAGG
      ACTCCAGGGGCCACAAGTGCCTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCC

      AlaHisLeuHisAlaProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAla
1801  TGGCTCACCTCCATGCTCCCACAGGCAGCGGCAAAAGCACCAAGGTCCCGGCTGCATATG
      ACCGAGTGGAGGTACGAGGGTGTCCGTCGCCGTTTTCGTGGTTCCAGGGCCGACGTATAC

      AlaGlnGlyTyrLysValLeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGly
1861  CAGCTCAGGGCTATAAGGTGCTAGTACTCAACCCCTCTGTTGCTGCAACACTGGGCTTTG
      GTCGAGTCCCGATATTCCACGATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAAC

      AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle
1921  GTGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAA
      CACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTT

      ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys
1981  TTACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGT
      AATGGTGACCGTCGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCA

      SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer
2041  GCTCGGGGGGCGCTTATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACAT
      CGAGCCCCCCGCGAATACTGTATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTA

      IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal
2101  CCATCTTGGGCATCGGCACTGTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTG
      GGTAGAACCCGTAGCCGTGACAGGAACTGGTTCGTCTCTGACGCCCCCGCTCTGACCAAC

      LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal
2161  TGCTCGCCACCGCCACCCCTCCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGGAGG
      ACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCC

      AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle
2221  TTGCTCTGTCCACCACCGGAGAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAA
      AACGAGACAGGTGGTGGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATT

      LysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAla
2281  TCAAGGGGGGGAGACATCTCATCTTCTGTCATTCAAAGAAGAAGTGCGACGAACTCGCCG
      AGTTCCCCCCCTCTGTAGAGTAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGC

      LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal
2341  CAAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCG
      GTTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGC

      IleProThrSerGlyAspValValValValAlaThrAspAlaLeuMetThrGlyTyrThr
2401  TCATCCCGACCAGCGGCGATGTTGTCGTCGTGGCAACCGATGCCCTCATGACCGGCTATA
      AGTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATAT

      GlyAspPheAspSerValIleAspCysAsnThrCysValThrGlnThrValAspPheSer
2461  CCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTGTCACCCAGACAGTCGATTTCA
      GGCCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTCTGTCAGCTAAAGT

      LeuAspProThrPheThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThr
2521  GCCTTGACCCTACCTTCACCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCCGCA
      CGGAACTGGGATGGAAGTGGTAACTCTGTTAGTGCGAGGGGGTCCTACGACAGAGGGCGT

      GlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGly
2581  CTCAACGTCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGG
      GAGTTGCAGCCCCGTCCTGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCC

      GluArgProSerGlyMetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCys
2641  GGGAGCGCCCCTCCGGCATGTTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCT
      CCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGA

      AlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThr
2701  GTGCTTGGTATGAGCTCACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACA
      CACGAACCATACTCGAGTGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGT
```

FIG. 32D

```
                ProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeu
2761 CCCCGGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCC
     GGGGCCCCGAAGGGCACACGGTCCTGGTAGAACTTAAAACCCTCCCGCAGAAATGTCCGG

                ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyr
2821 TCACTCATATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTT
     AGTGAGTATATCTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAA

                LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAsp
2881 ACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGG
     TGGACCATCGCATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCC

                GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu
2941 ACCAGATGTGGAAGTGTTTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGC
     TGGTCTACACCTTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACG

                TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle
3001 TATACAGACTGGGCGCTGTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACA
     ATATGTCTGACCCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGT

                MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly
3061 TCATGACATGCATGTCGGCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCG
     AGTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGC

                ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg
3121 GCGTCCTGGCTGCTTTGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCA
     CGCAGGACCGACGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGT

                ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe
3181 GGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGT
     CCCAGCAGAACAGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCA

                AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla
3241 TCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCG
     AGCTACTCTACCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGC

                GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal
3301 CCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGG
     GGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCC

                IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet
3361 TTATCGCCCCTGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATA
     AATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTAT

                TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro
3421 TGTGGAACTTCATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACC
     ACACCTTGAAGTAGTCACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGG

                AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln
3481 CCGCCATTGCTTCATTGATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCC
     GGCGGTAACGAAGTAACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGG

                ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla
3541 AAACCCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTG
     TTTGGGAGGAGAAGTTGTATAACCCCCCCACCCACCGACGGGTCGAGCGGCGGGGGCCAC

                AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly
3601 CCGCTACTGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGG
     GGCGATGACGGAAACACCCGCGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACC

                LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla
3661 GGAAGGTCCTCATAGACATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGG
     CCTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACC

                PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla
3721 CATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCG
     GTAAGTTCTAGTACTCGCCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGC
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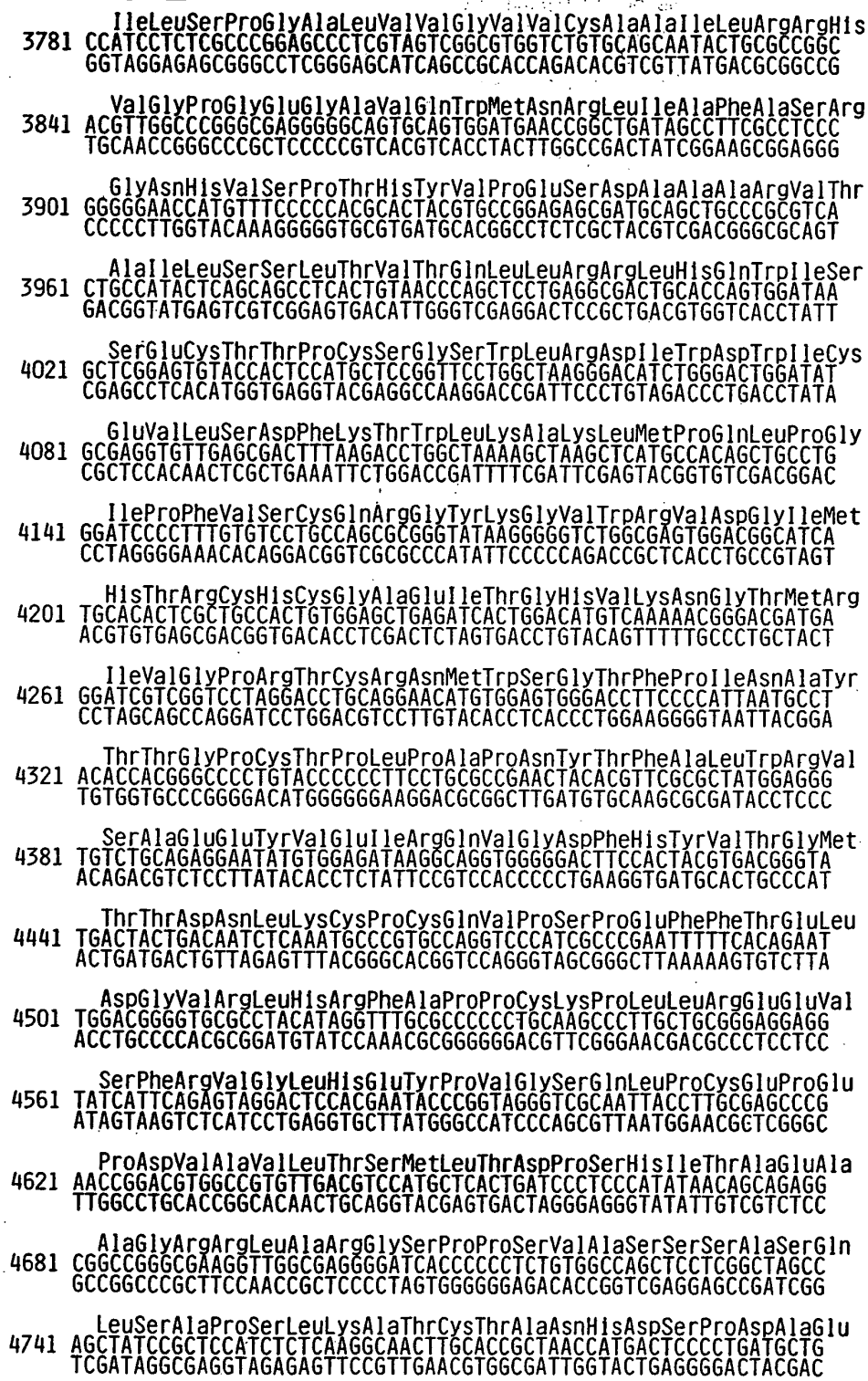
FIG. 32E



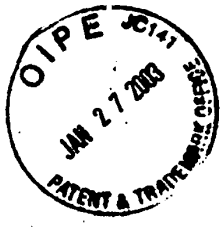


FIG. 32F

```
                LeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGlu
4801 AGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGGCGGCAACATCACCAGGGTTG
     TCGAGTATCTCCGGTTGGAGGATACCTCCGTCCTCTACCCGCCGTTGTAGTGGTCCCAAC

                SerGluAsnLysValValIleLeuAspSerPheAspProLeuValAlaGluGluAspGlu
4861 AGTCAGAAAACAAAGTGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCGGAGGAGGACG
     TCAGTCTTTTGTTTCACCACTAAGACCTGAGGAAGCTAGGCGAACACCGCCTCCTCCTGC

                ArgGluIleSerValProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeu
4921 AGCGGGAGATCTCCGTACCCGCAGAAATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCC
     TCGCCCTCTAGAGGCATGGGCGTCTTTAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGG

                ProValTrpAlaArgProAspTyrAsnProProLeuValGluThrTrpLysLysProAsp
4981 TGCCCGTTTGGGCGCGGCCGGACTATAACCCCCCGCTAGTGGAGACGTGGAAAAAGCCCG
     ACGGGCAAACCCGCGCCGGCCTGATATTGGGGGGCGATCACCTCTGCACCTTTTTCGGGC

                TyrGluProProValValHisGlyCysProLeuProProProLysSerProProValPro
5041 ACTACGAACCACCTGTGGTCCATGGCTGTCCGCTTCCACCTCCAAAGTCCCCTCCTGTGC
     TGATGCTTGGTGGACACCAGGTACCGACAGGCGAAGGTGGAGGTTTCAGGGGAGGACACG

                ProProArgLysLysArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAla
5101 CTCCGCCTCGGAAGAAGCGGACGGTGGTCCTCACTGAATCAACCCTATCTACTGCCTTGG
     GAGGCGGAGCCTTCTTCGCCTGCCACCAGGAGTGACTTAGTTGGGATAGATGACGGAACC

                GluLeuAlaThrArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThr
5161 CCGAGCTCGCCACCAGAAGCTTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATA
     GGCTCGAGCGGTGGTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCCGCTGTTAT

                ThrThrSerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerTyr
5221 CGACAACATCCTCTGAGCCCGCCCCTTCTGGCTGCCCCCCCGACTCCGACGCTGAGTCCT
     GCTGTTGTAGGAGACTCGGGCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGA

                SerSerMetProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrp
5281 ATTCCTCCATGCCCCCCCTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTCAT
     TAAGGAGGTACGGGGGGGACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTA

                SerThrValSerSerGluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSer
5341 GGTCAACGGTCAGTAGTGAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCTTACT
     CCAGTTGCCAGTCATCACTCCGGTTGCGCCTCCTACAGCACACGACGAGTTACAGAATGA

                TrpThrGlyAlaLeuValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAla
5401 CTTGGACAGGCGCACTCGTCACCCCGTGCGCCGCGGAAGAACAGAAACTGCCCATCAATG
     GAACCTGTCCGCGTGAGCAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTAC

                LeuSerAsnSerLeuLeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAla
5461 CACTAAGCAACTCGTTGCTACGTCACCACAATTTGGTGTATTCCACCACCTCACGCAGTG
     GTGATTCGTTGAGCAACGATGCAGTGGTGTTAAACCACATAAGGTGGTGGAGTGCGTCAC

                CysGlnArgGlnLysLysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGln
5521 CTTGCCAAAGGCAGAAGAAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACC
     GAACGGTTTCCGTCTTCTTTCAGTGTAAACTGTCTGACGTTCAAGACCTGTCGGTAATGG

                AspValLeuLysGluValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerVal
5581 AGGACGTACTCAAGGAGGTTAAAGCAGCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCG
     TCCTGCATGAGTTCCTCCAATTTCGTCGCCGCAGTTTTCACTTCCGATTGAACGATAGGC

                GluGluAlaCysSerLeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAla
5641 TAGAGGAAGCTTGCAGCCTGACGCCCCCACACTCAGCCAAATCCAAGTTTGGTTATGGGG
     ATCTCCTTCGAACGTCGGACTGCGGGGGTGTGAGTCGGTTTAGGTTCAAACCAATACCCC

                LysAspValArgCysHisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAsp
5701 CAAAAGACGTCCGTTGCCATGCCAGAAAGGCCGTAACCCACATCAACTCCGTGTGGAAAG
     GTTTTCTGCAGGCAACGGTACGGTCTTTCCGGCATTGGGTGTAGTTGAGGCACACCTTTC

                LeuLeuGluAspAsnValThrProIleAspThrThrIleMetAlaLysAsnGluValPhe
5761 ACCTTCTGGAAGACAATGTAACACCAATAGACACTACCATCATGGCTAAGAACGAGGTTT
     TGGAAGACCTTCTGTTACATTGTGGTTATCTGTGATGGTAGTACCGATTCTTGCTCCAAA
```

FIG. 32G

```
                CysValGlnProGluLysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeu
5821 TCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATC
     AGACGCAAGTCGGACTCTTCCCCCCAGCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAG

                GlyValArgValCysGluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAla
5881 TGGGCGTGCGCGTGTGCGAAAAGATGGCTTTGTACGACGTGGTTACAAAGCTCCCCTTGG
     ACCCGCACGCGCACACGCTTTTCTACCGAAACATGCTGCACCAATGTTTCGAGGGGAACC

                ValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuVal
5941 CCGTGATGGGAAGCTCCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCCTCG
     GGCACTACCCTTCGAGGATGCCTAAGGTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGC

                GlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAspThrArgCysPheAsp
6001 TGCAAGCGTGGAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGATACCCGCTGCTTTG
     ACGTTCGCACCTTCAGGTTCTTTTGGGGTTACCCCAAGAGCATACTATGGGCGACGAAAC

                SerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeu
6061 ACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAATGTTGTGACC
     TGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTTACAACACTGG

                AspProGlnAlaArgValAlaIleLysSerLueThrGluArgLeuTyrValGlyGlyPro
6121 TCGACCCCCAAGCCCGCGTGGCCATCAAGTCCCTCACCGAGAGGCTTTATGTTGGGGGCC
     AGCTGGGGGTTCGGGCGCACCGGTAGTTCAGGGAGTGGCTCTCCGAAATACAACCCCCGG

                LeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeu
6181 CTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCGAGCGGCGTAC
     GAGAATGGTTAAGTTCCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGCTCGCCGCATG

                ThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAla
6241 TGACAACTAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAG
     ACTGTTGATCGACACCATTGTGGGAGTGAACGATGTAGTTCCGGGCCCGTCGGACAGCTC

                AlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuValValIleCysGlu
6301 CCGCAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTG
     GGCGTCCCGAGGTCCTGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACAC

                SerAlaGlyValGlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArg
6361 AAAGCGCGGGGGTCCAGGAGGACGCGGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCA
     TTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCGGACTCTCGGAAGTGCCTCCGATACTGGT

                TyrSerAlaProProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSer
6421 GGTACTCCGCCCCCCCTGGGGACCCCCCACAACCAGAATACGACTTGGAGCTCATAACAT
     CCATGAGGCGGGGGGGACCCCTGGGGGGTGTTGGTCTTATGCTGAACCTCGAGTATTGTA

                CysSerSerAsnValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThr
6481 CATGCTCCTCCAACGTGTCAGTCGCCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCA
     GTACGAGGAGGTTGCACAGTCAGCGGGTGCTGCCGCGACCTTTCTCCCAGATGATGGAGT

                ArgAspProThrThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProVal
6541 CCCGTGACCCTACAACCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAG
     GGGCACTGGGATGTTGGGGGGAGCGCTCTCGACGCACCCTCTGTCGTTCTGTGTGAGGTC

                AsnSerTrpLeuGlyAsnIleIleMetPheAlaProThrLeuTrpAlaArgMetIleLeu
6601 TCAATTCCTGGCTAGGCAACATAATCATGTTTGCCCCCACACTGTGGGCGAGGATGATAC
     AGTTAAGGACCGATCCGTTGTATTAGTACAAACGGGGGTGTGACACCCGCTCCTACTATG

                MetThrHisPhePheSerValLeuIleAlaArgAspGlnLeuGluGlnAlaLeuAspCys
6661 TGATGACCCATTTCTTTAGCGTCCTTATAGCCAGGGACCAGCTTGAACAGGCCCTCGATT
     ACTACTGGGTAAAGAAATCGCAGGAATATCGGTCCCTGGTCGAACTTGTCCGGGAGCTAA

                GluIleTyrGlyAlaCysTyrSerIleGluProLeuAspLeuProProIleIleGlnArg
6721 GCGAGATCTACGGGGCCTGCTACTCCATAGAACCACTTGATCTACCTCCAATCATTCAAA
     CGCTCTAGATGCCCCGGACGATGAGGTATCTTGGTGAACTAGATGGAGGTTAGTAAGTTT

                Leu
6781 GACTC
     CTGAG
```

FIG. 33

Lane Number	Chimp Reference Number	Infection Type	Sample date (days) (0=inoculation day)	ALT (alanine) aminotransferase level in sera)mμ/ml)
1	1	NANB	0	0
2	1	NANB	76	71
3	1	NANB	118	19
4	1	NANB	154	N/A
5	2	NANB	0	0
6	2	NANB	21	52
7	2	NANB	73	13
8	2	NANB	138	N/A
9	3	NANB	0	8
10	3	NANB	43	205
11	3	NANB	53	14
12	3	NANB	159	6
13	4	NANB	-3	11
14	4	NANB	55	132
15	4	NANB	83	N/A
16	4	NANB	140	N/A
17	5	HAV	0	4
18	5	HAV	25	147
19	5	HAV	40	18
20	5	HAV	268	5
21	6	HAV	-8	N/A
22	6	HAV	15	100
23	6	HAV	41	10
24	6	HAV	129	N/A
26	7	HAV	0	7
27	7	HAV	22	83
28	7	HAV	115	5
29	7	HAV	139	N/A
30	8	HAV	0	15
31	8	HAV	26	130
32	8	HAV	74	8
33	8	HAV	205	5
34	9	HBV	-290	N/A
35	9	HBV	379	9
36	9	HBV	435	6
37	10	HBV	0	8
38	10	HBV	111-118 (pool)	96-156 (pool)
39	10	HBV	205	9
40	10	HBV	240	13
41	11	HBV	0	11
42	11	HBV	28-56 (pool)	8-100 (pool)
43	11	HBV	169	9
44	11	HBV	223	10

FIG. 33A

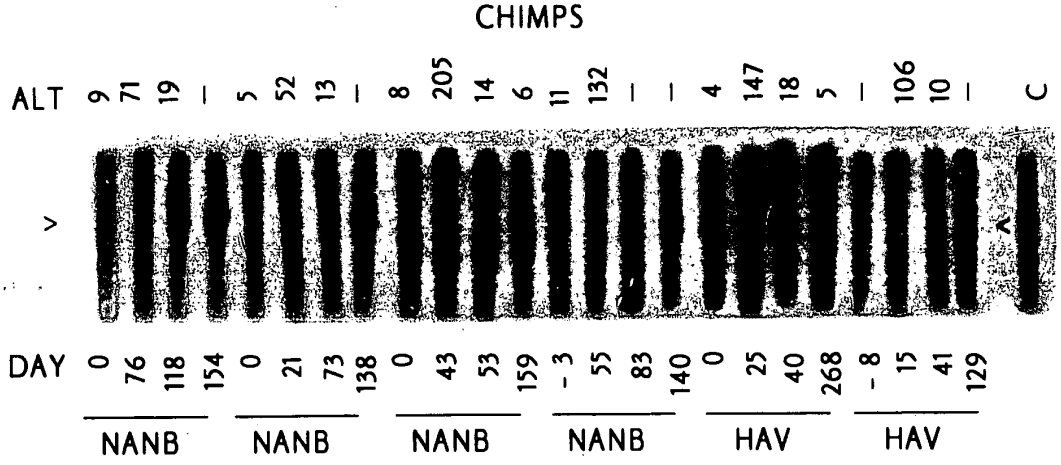


FIG. 33B

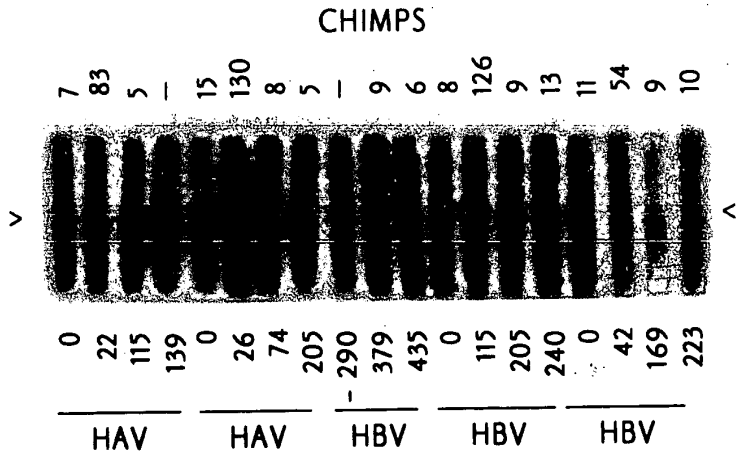


FIG. 34

Lane Number	Patient Reference Number	Diagnosis	ALT Level (mμ/ml)
1	1[1]	NANB	1354
2	1[1]	NANB	31
3	2[1]	NANB	14
4	2[1]	NANB	79
5	2[1]	NANB	26
6	3[1]	NANB	78
7	3[1]	NANB	87
8	3[1]	NANB	25
9	4[1]	NANB	60
10	4[1]	NANB	13
11	5[1]	NANB	298
12	5[1]	NANB	101
13	6[1]	NANB	474
14	6[1]	NANB	318
15	7[1]	NANB	20
16	7[1]	NANB	163
17	8[1]	NANB	44
18	8[1]	NANB	50
19	9	NANB	N/A
20	10	NANB	N/A
21	11	NANB	N/A
22	12	Normal	N/A
23	13	Normal	N/A
24	14	Normal	N/A
26	30174	Normal	N/A
27	30105	Normal	N/A
28	30072	Normal	N/A
29	30026	Normal	N/A
30	30146	Normal	N/A
31	30250	Normal	N/A
32	30071	Normal	N/A
33	15	AcuteHAV	N/A
34	16	AcuteHAV	N/A
35	17	AcuteHAV	N/A
36	18	AcuteHAV	N/A
37	48088	AcuteHAV	N/A
38	47288	AcuteHAV	N/A
39	47050	AcuteHAV	N/A
40	46997	AcuteHAV	N/A
41	19	Convalescent HBV	N/A
42	20	(anti-HBSag+ve;	N/A
43	21	anti-HBCag+ve)	N/A
44	22	(anti-HBSag+ve;	N/A
45	23	anti-HBCag+ve)	N/A
46	24	(anti-HBSag+ve;	N/A
47	25	anti-HBCag+ve)	N/A
48	26	(anti-HBSag+ve;	N/A
49	27	anti-HBSag+ve)	N/A

[1]Sequential serum samples were assayed from these patients

FIG. 34A

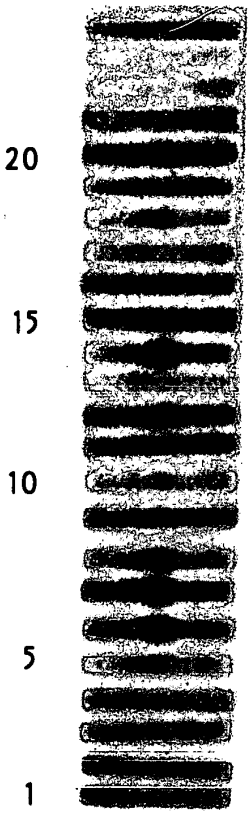


FIG. 34B

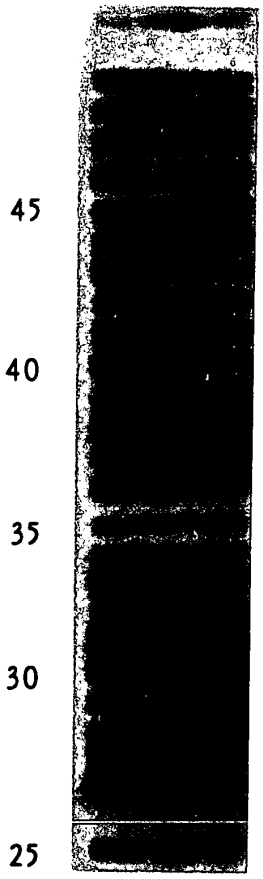


FIG. 35

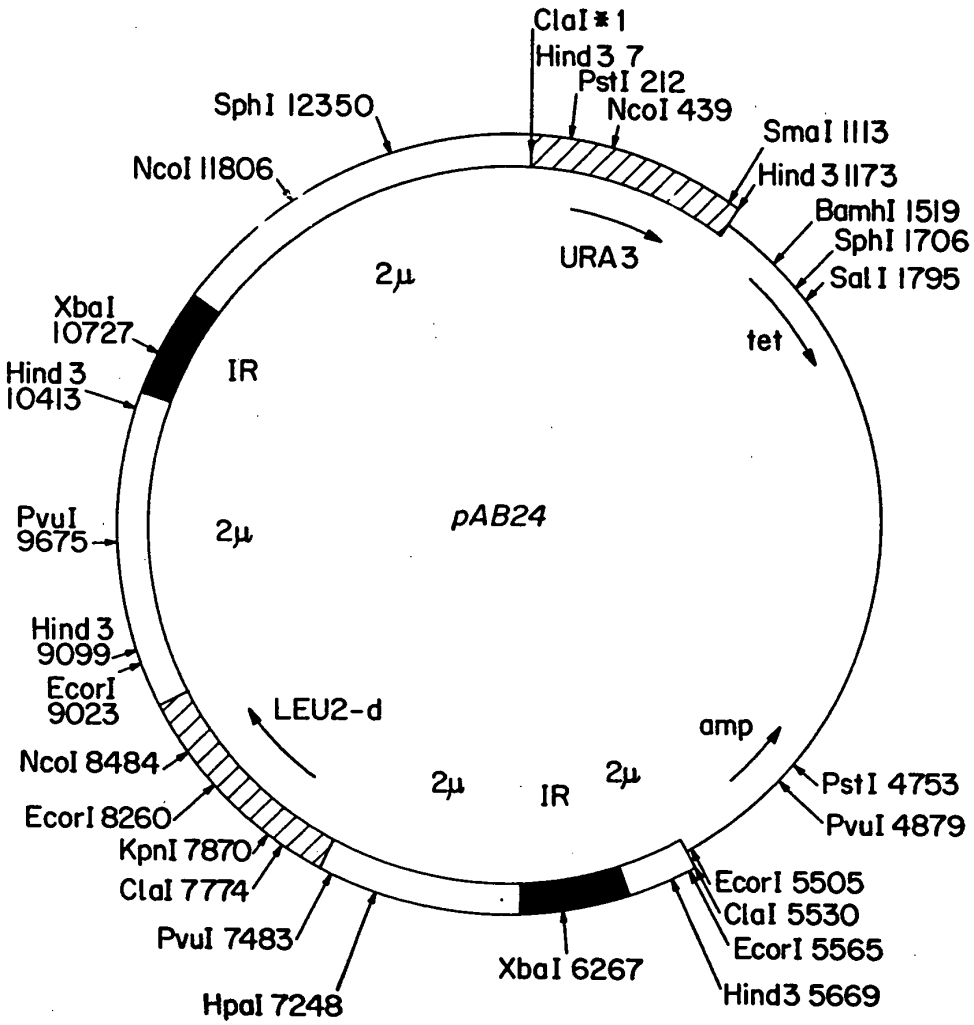


FIG. 36A

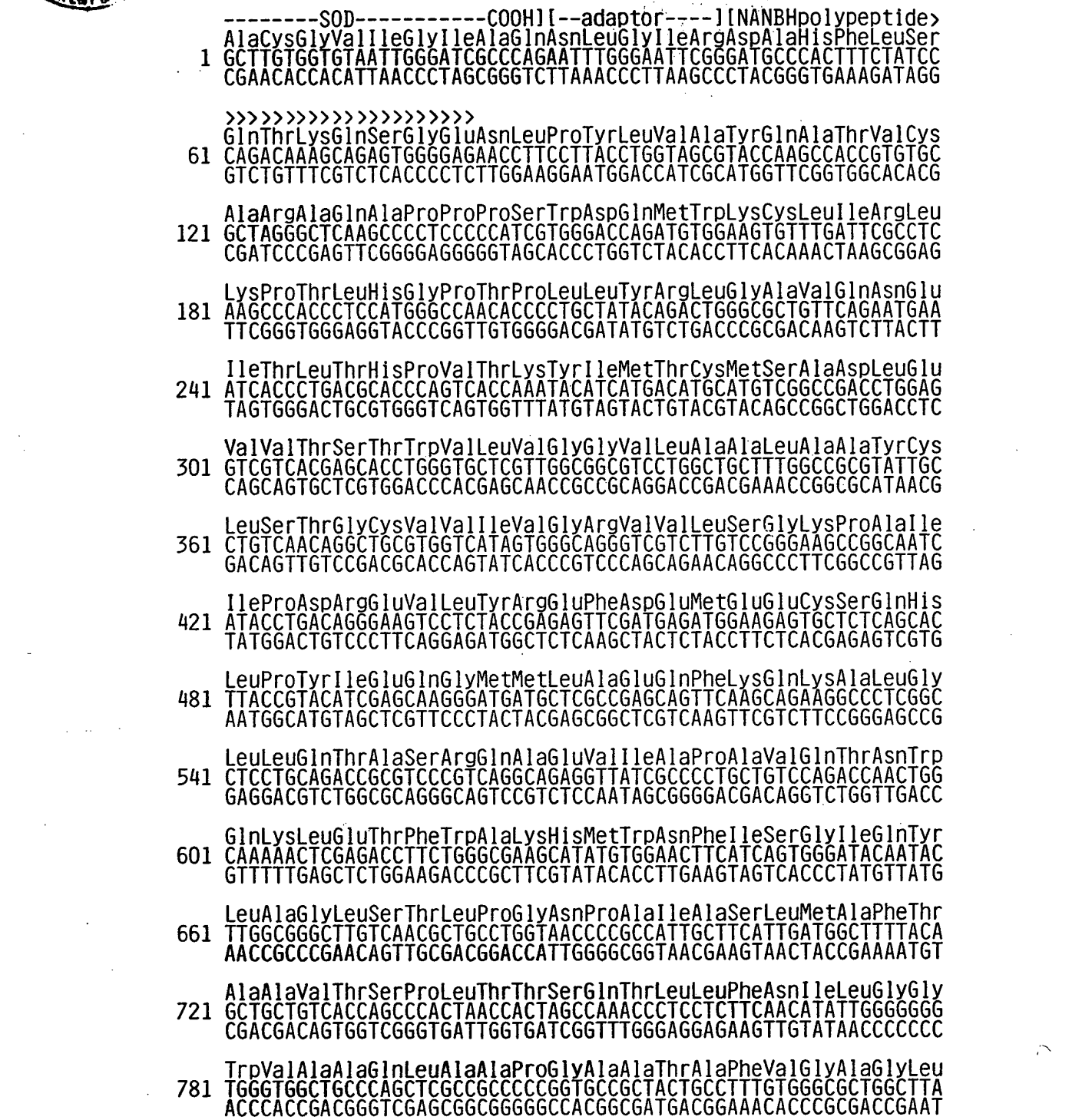


FIG. 36B

FIG. 37A

FIG. 37B

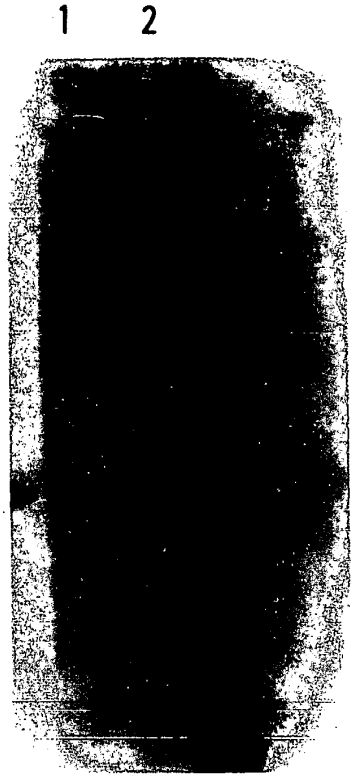


FIG. 38

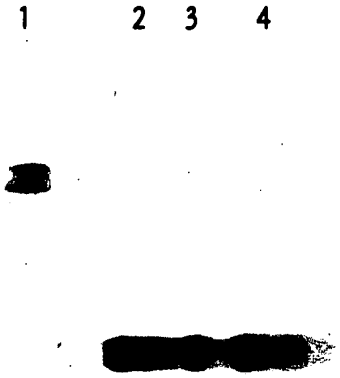


FIG. 40

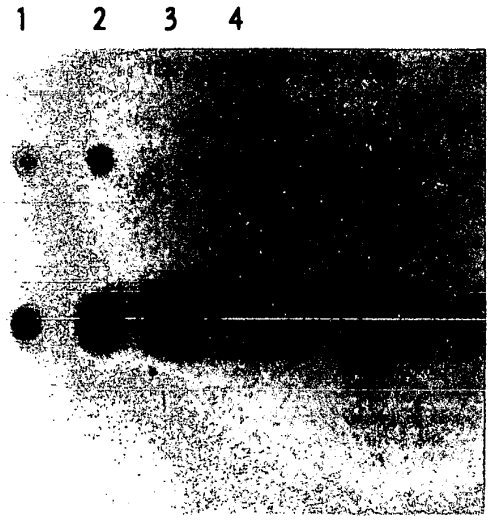


FIG. 39

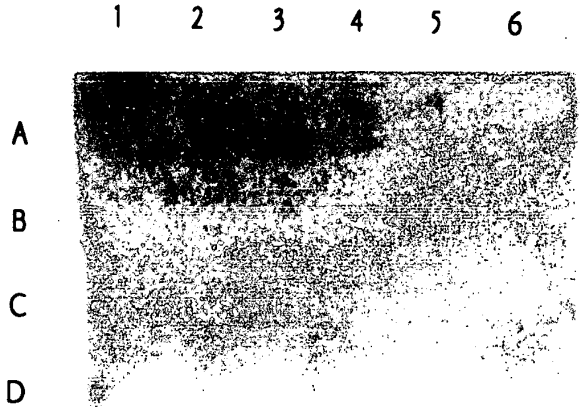


FIG. 41A

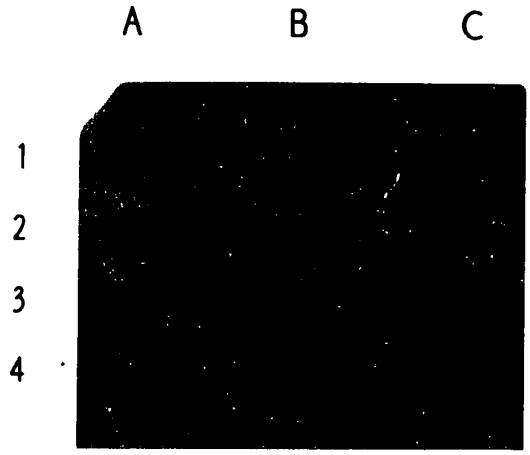


FIG. 41B

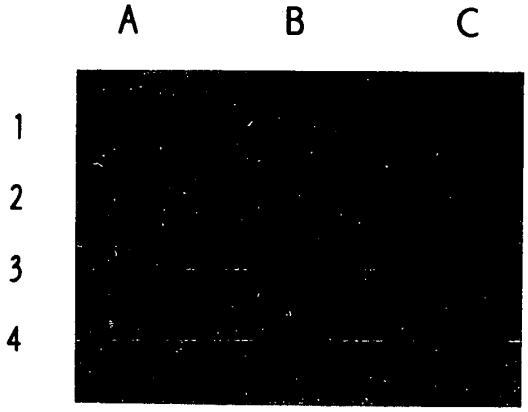


FIG. 42A

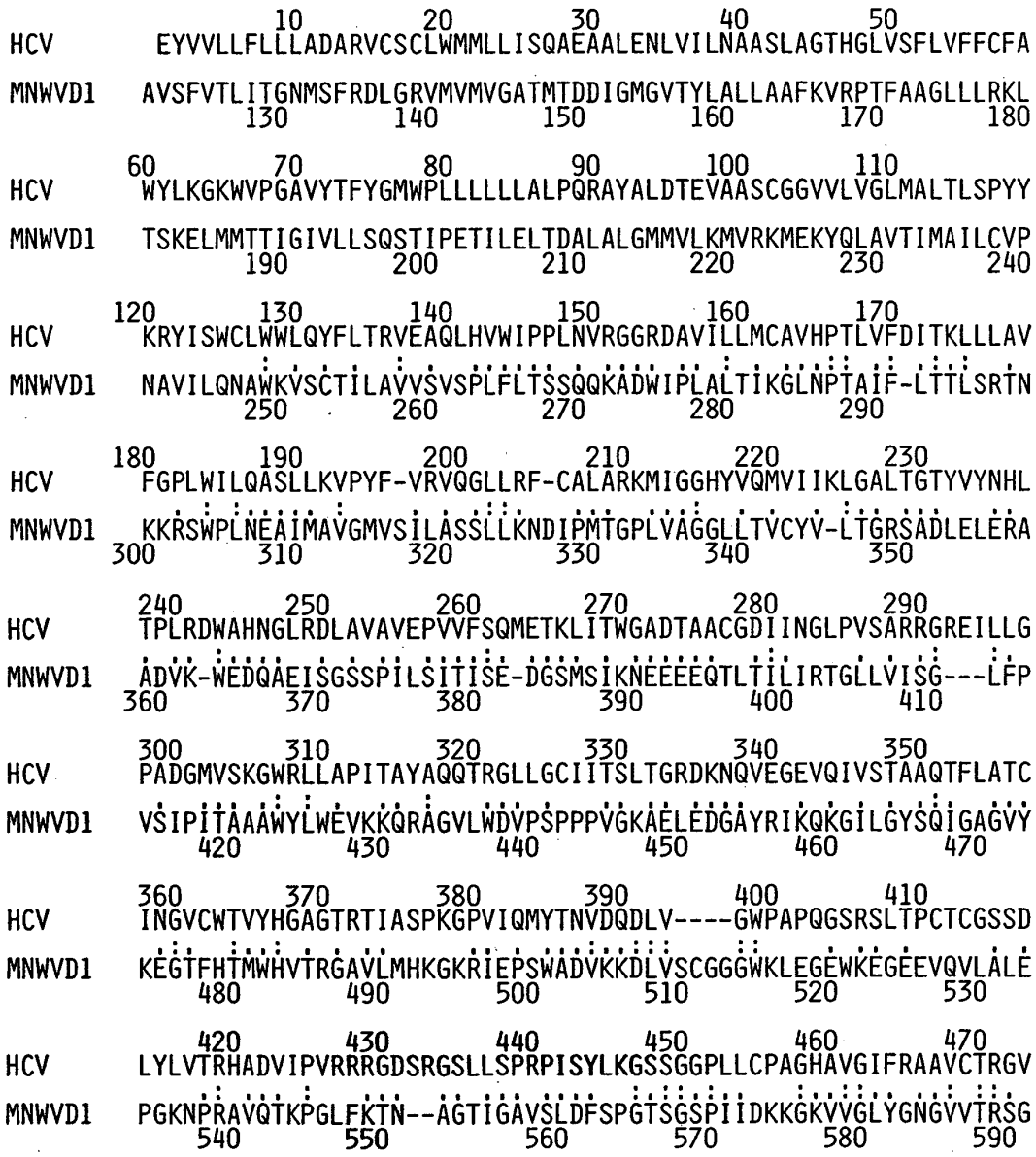


FIG. 42B

```
                480       490       500       510       520       530
HCV      AKAVDFIPVENLETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGSGKS--TKVPAAYAAQ
         :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
MNWVD1   AYVSAIAQTEK--SIEDNPEIEDDIFRK---RKLTIMDLHPGAGKTKRYLPAIVRGAIKR
                600       610       620       630       640

                540       550       560       570       580
HCV      GYKVLVLNPS--VAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGC
         :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
MNWVD1   GLRTLILAPTRVVAAEMEEALRGLPIRYQTPAIRAEHTGREIVDLMCHATFTMRLL-SPV
                650       660       670       680       690       700

              590       600       610       620       630       640
HCV        SGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV
                X                                                   V
MNWVD1     RVPNYNLIIMDEAHFTDPASIAARGYISTRVE-MGEAAGIFMTATPPGSRD-PFPQSNAP
                710       720       730       740       750       760

              650       660       670       680       690       700
HCV        ALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSV
           :  :  :  :
MNWVD1     IMDEERETPERSWSSGHEWVTDFKGKTVWFVPSIKAGNDTAACLRKNGKKVTQLSRKTFD
                770       780       790       800       810       820

            710       720       730       740       750       760
HCV        IPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRT
MNWVD1     SEYVKTRTNDWNFVVTTDISEMGANFKAERVIDPRRCMKPVILTDGEERVILAGPMPVTH
                830       840       850       860       870       880

            770       780       790       800       810       820
HCV        QRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT
MNWVD1     SS
```

FIG. 43

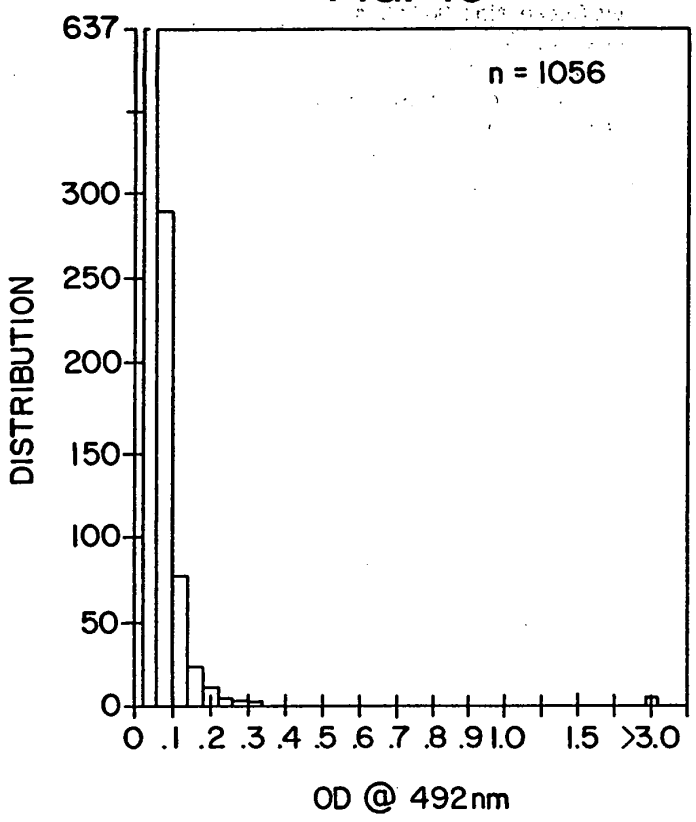


FIG. 44

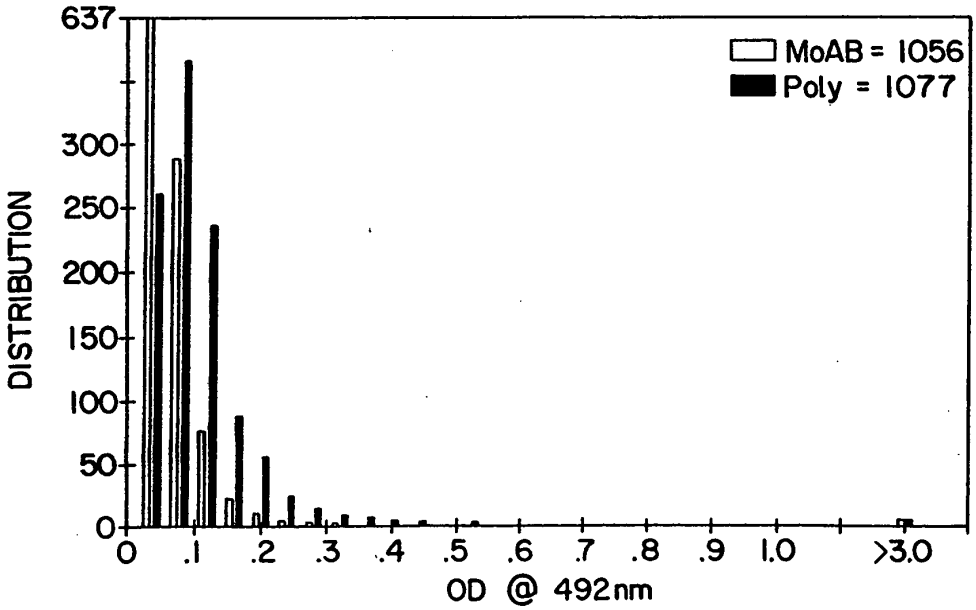


FIG. 45

Name	Common Sequence	Variable Sequence
5'-3-1	AAGCTTGATCGAATTC	CGATCTTGC
-2		CGATCCTGC
-3		CGATCATGC
-4		CGATCGTGC
-5		CGAAGTTGC
-6		CGAAGCTGC
-7		AGATCTTGC
-8		AGATCCTGC
-9		AGATCATGC
-10		AGATCGTGC
-11		AGAAGTTGC
-12		AGAAGCTGC
-13		CGATCTTGT
-14		CGATCCTGT
-15		CGATCATGT
-16		CGATCGTGT
-17		CGAAGTTGT
-18		CGAAGCTGT
-19		AGATCTTGT
-20		AGATCCTGT
-21		AGATCATGT
-22		AGATCGTGT
-23		AGAAGTTGT
-24		AGAAGCTGT
-25		CGCTCTTGC
-26		CGCTCCTGC
-27		CGCTCATGC
-28		CGCTCGTGC
-29		CGCAGTTGC
-30		CGCAGCTGC
-31		CGCTCTTGT
-32		CGCTCCTGT
-33		CGCTCATGT
-34		CGCTCGTGT
-35		CGCAGTTGT
-36		CGCAGCTGT

FIG. 46A

```
     GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly
   1 CAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGG
     GTCCGACAGGACTCTCCGATCGGTCGACGGCTGGGGAATGGCTAAAACTGGTCCCGACCC

     ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro
  61 GCCCTATCAGTTATGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCTGGCACTACC
     CGGGATAGTCAATACGGTTGCCTTCGCCGGGGCTGGTCGCGGGGATGACGACCGTGATGG

     ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr
 121 CCCCAAAACCTTGCGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTATATTGCTTCA
     GGGGTTTTGGAACGCCATAACACGGGCGCTTCTCACACACACCAGGCCATATAACGAAGT

     ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly
 181 CTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCTACAGCTGGG
     GAGGGTCGGGGCACCACCACCCTTGCTGGCTGTCCAGCCCGCGCGGGTGGATGTCGACCC

     GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe
 241 GTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGT
     CACTTTTACTATGCCTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCA

     GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal
 301 TCGGTTGTACCTGGATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGCCTCCTTGTG
     AGCCAACATGGACCTACTTGAGTTGACCTAAGTGGTTTCACACGCCTCGCGGAGGAACAC
```

FIG. 46B

```
      IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro
361 TCATCGGAGGGGCGGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCCGCAAGCATC
    AGTAGCCTCCCCGCCCGTTGTTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCGTAG

      AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp
421 CGGACGCCACATACTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCG
    GCCTGCGGTGTATGAGAGCCACGCCGAGGCCAGGGACCTAGTGTGGGTCCACGGACCAGC

                                                    ----------

      TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg
481 ACTACCCGTATAGGCTTTGGCATTATCCTTGTACCATCAACT ACTATATTTAAAATCA
    TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGATATAAATTTTAGT

    ------------------------------------------------------------

      MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu
541 GGATGTACGTGGGAGGGGTCGAGCACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCG
    CCTACATGCACCCTCCCCAGCTCGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGC

    ------------------------------------------------------------

      ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr
601 AACGTTGCGATCTGGAAGATAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA
    TTGCAACGCTAGACCTTCTATCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGAT

    ------------------------------------------ ----------------

      GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle
661 CACAGTGGCAGGTCCTCCCGTGTTCCTTCACAACCCTGCCAGCCTTGTCCACCGGCCTCA
    GTGTCACCGTCCAGGAGGGCACAAGGAAGTGTTGGGACGGTCGGAACAGGTGGCCGGAGT
```

FIG. 46C

```
     -----Overlap with Combined ORF of DNAs 12f through 15e------
       HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla
721  TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCG
     AGGTGGAGGTGGTCTTGTAACACCTGCACGTCATGAACATGCCCCACCCCAGTTCGTAGC

     ------------------------------------------------------------

       SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArg
781  CGTCCTGGGCCATTAAGTGGGAGTACGTCGTCCTCCTGTTCCTTCTGCTTGCAGACGCGC
     GCAGGACCCGGTAATTCACCCTCATGCAGCAGGAGGACAAGGAAGACGAACGTCTGCGCG

     ------------------------------------------------------------

       ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn
841  GCGTCTGCTCCTGCTTGTGGATGATGCTACTCATATCCCAAGCGGAAGCGGCTTTGGAGA
     CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCCTTCGCCGAAACCTCT

     ------------------------------------------------------------

       LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal
901  ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCG
     TGGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGC

     ------------------------------------------------------------

       PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPhe
961  TGTTCTTCTGCTTTGCATGGTATCTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCT
     ACAAGAAGACGAAACGTACCATAGACTTCCCATTCACCCACGGGCCTCGCCAGATGTGGA
```

FIG. 46D

FIG. 47A

```
                GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly
  1 CAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGG
    GTCCGACAGGACTCTCCGATCGGTCGACGGCTGGGGAATGGCTAAAACTGGTCCCGACCC

                ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro
 61 GCCCTATCAGTTATGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCTGGCACTACC
    CGGGATAGTCAATACGGTTGCCTTCGCCGGGGCTGGTCGCGGGGATGACGACCGTGATGG

                ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr
121 CCCCAAAACCTTGCGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTATATTGCTTCA
    GGGGTTTTGGAACGCCATAACACGGGCGCTTCTCACACACACCAGGCCATATAACGAAGT

                ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly
181 CTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCTACAGCTGGG
    GAGGGTCGGGGCACCACCACCCTTGCTGGCTGTCCAGCCCGCGCGGGTGGATGTCGACCC

                GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe
241 GTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGT
    CACTTTTACTATGCCTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCA

                GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal
301 TCGGTTGTACCTGGATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGCCTCCTTGTG
    AGCCAACATGGACCTACTTGAGTTGACCTAAGTGGTTTCACACGCCTCGCGGAGGAACAC

                IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro
361 TCATCGGAGGGGCGGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCCGCAAGCATC
    AGTAGCCTCCCCGCCCGTTGTTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCGTAG

                AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp
421 CGGACGCCACATACTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCG
    GCCTGCGGTGTATGAGAGCCACGCCGAGGCCAGGGACCTAGTGTGGGTCCACGGACCAGC

                TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg
481 ACTACCCGTATAGGCTTTGGCATTATCCTTGTACCATCAACTACACCATATTTAAAATCA
    TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTTAGT

                MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu
541 GGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCG
    CCTACATGCACCCTCCCCAGCTTGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGC

                ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr
601 AACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA
    TTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGAT

                GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle
661 CACAGTGGCAGGTCCTCCCGTGTTCCTTCACAACCCTACCAGCCTTGTCCACCGGCCTCA
    GTGTCACCGTCCAGGAGGGCACAAGGAAGTGTTGGGATGGTCGGAACAGGTGGCCGGAGT

                HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla
721 TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCG
    AGGTGGAGGTGGTCTTGTAACACCTGCACGTCATGAACATGCCCCACCCCAGTTCGTAGC

                SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArg
781 CGTCCTGGGCCATTAAGTGGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTGCAGACGCGC
    GCAGGACCCGGTAATTCACCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCG

                ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn
841 GCGTCTGCTCCTGCTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGA
    CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCT

                LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal
901 ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCG
    TGGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGC
```

FIG. 47B

```
                PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPhe
961  TGTTCTTCTGCTTTGCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCT
     ACAAGAAGACGAAACGTACCATAAACTTCCCATTCACCCACGGGCCTCGCCAGATGTGGA

                TyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeu
1021 TCTACGGGATGTGGCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGC
     AGATGCCCTACACCGGAGAGGAGGACGAGGACAACCGCAACGGGGTCGCCCGCATGCGCG

                AspThrGluValAlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThr
1081 TGGACACGGAGGTGGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGA
     ACCTGTGCCTCCACCGGCGCAGCACACCGCCACAACAAGAGCAGCCCAACTACCGCGACT

                LeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeu
1141 CTCTGTCACCATATTACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTC
     GAGACAGTGGTATAATGTTCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAG

                ThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArg
1201 TGACCAGAGTGGAAGCGCAACTGCACGTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGC
     ACTGGTCTCACCTTCGCGTTGACGTGCACACCTAAGGGGGGGAGTTGCAGGCTCCCCCCG

                AspAlaValIleLeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLys
1261 GCGACGCCGTCATCTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCA
     CGCTGCGGCAGTAGAATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGT

                LeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValPro
1321 AATTGCTGCTGGCCGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTAC
     TTAACGACGACCGGCAGAAGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTCATG

                TyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGly
1381 CCTACTTTGTGCGCGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCG
     GGATGAAACACGCGCAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCCTTCTACTAGC

                GlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyr
1441 GAGGCCATTACGTGCAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTT
     CTCCGGTAATGCACGTTTACCAGTAGTAATTCAATCCCCGCGAATGACCGTGGATACAAA

                AsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAla
1501 ATAACCATCTCACTCCTCTTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGG
     TATTGGTAGAGTGAGGAGAAGCCCTGACCCGCGTGTTGCCGAACGCTCTAGACCGGCACC

                ValGluProValValPheSerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThr
1561 CTGTAGAGCCAGTCGTCTTCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATA
     GACATCTCGGTCAGCAGAAGAGGGTTTACCTCTGGTTCGAGTAGTGCACCCCCCGTCTAT

                AlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArgArgGlyArgGluIle
1621 CCGCCGCGTGCGGTGACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGA
     GGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGGCGGGCGTCCCCGGCCCTCT

                LeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThr
1681 TACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCA
     ATGACGAGCCCGGTCGGCTACCTTACCAGAGGTTCCCCACCTCCAACGACCGCGGGTAGT

                AlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArg
1741 CGGCGTACGCCCAGCAGACAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCC
     GCCGCATGCGGGTCGTCTGTTCCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGG

                AspLysAsnGlnValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeu
1801 GGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCC
     CCCTGTTTTTGGTTCACCTCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAGG

                AlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIle
1861 TGGCAACGTGCATCAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCA
     ACCGTTGCACGTAGTTACCCCACACGACCTGACAGATGGTGCCCCGGCCTTGCTCCTGGT

                AlaSerProLysGlyProValIleGlnMetTyrThrAsnValAspGlnAspLeuValGly
1921 TCGCGTCACCCAAGGGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGG
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FIG. 47C

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                TrpProAlaProGlnGlySerArgSerLeuThrProCysThrCysGlySerSerAspLeu
1981 GCTGGCCCGCTCCGCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACC
     CGACCGGGCGAGGCGTTCCATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGG

                TyrLeuValThrArgHisAlaAspValIleProValArgArgArgGlyAspSerArgGly
2041 TTTACCTGGTCACGAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGG
     AAATGGACCAGTGCTCCGTGCGGCTACAGTAAGGGCACGCGGCCGCCCCACTATCGTCCC

                SerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeu
2101 GCAGCCTGCTGTCGCCCCGGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGGTCCGCTGT
     CGTCGGACGACAGCGGGGCCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCCAGGCGACA

                CysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAla
2161 TGTGCCCCGCGGGGCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGG
     ACACGGGGCGCCCCGTGCGGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTCACC

                LysAlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPhe
2221 CTAAGGCGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGT
     GATTCCGCCACCTGAAATAGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACA

                ThrAspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAla
2281 TCACGGATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATG
     AGTGCCTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTAC

                ProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLys
2341 CTCCCACAGGCAGCGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATA
     GAGGGTGTCCGTCGCCGTTTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATAT

                ValLeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLys
2401 AGGTGCTAGTACTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCA
     TCCACGATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGT

                AlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerPro
2461 AGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCC
     TCCGAGTACCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGG

                IleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyr
2521 CCATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTT
     GGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAA

                AspIleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGly
2581 ATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCG
     TACTGTATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGC

                ThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThr
2641 GCACTGTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCA
     CGTGACAGGAACTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGT

                ProProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThr
2701 CCCCTCCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCA
     GGGGAGGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGT

                GlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHis
2761 CCGGAGAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGAC
     GGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTG

                LeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeu
2821 ATCTCATCTTCTGTCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCAT
     TAGAGTAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTA

                GlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGly
2881 TGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCG
     ACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGC

                AspValValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSer
2941 GCGATGTTGTCGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACT
     CGCTACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGA
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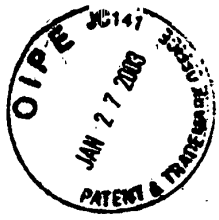

FIG. 47D

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                ValIleAspCysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPhe
3001 CGGTGATAGACTGCAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCT
     GCCACTATCTGACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGA

                ThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg
3061 TCACCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCA
     AGTGGTAACTCTGTTAGTGCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGT

                ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly
3121 GGACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCG
     CCTGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGC

                MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu
3181 GCATGTTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGC
     CGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCG

                ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal
3241 TCACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCG
     AGTGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGC

                CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla
3301 TGTGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATG
     ACACGGTCCTGGTAGAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTAC

                HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln
3361 CCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACC
     GGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGG

                AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys
3421 AAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGT
     TTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCA

                LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla
3481 GTTTGATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCG
     CAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGC

                ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer
3541 CTGTTCAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGT
     GACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACA

                AlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeu
3601 CGGCCGACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTT
     GCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAA

                AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly
3661 TGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCG
     ACCGGCGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGC

                LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu
3721 GGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAG
     CCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTC

                CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln
3781 AGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGC
     TCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCG

                LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal
3841 AGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTG
     TCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGAC

                GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer
3901 TCCAGACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCA
     AGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGT

                GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu
3961 GTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCAT
     CACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTA
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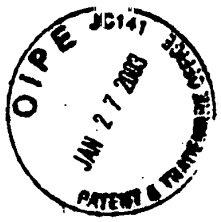

FIG. 47E

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          MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn
4021 TGATGGCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCA
     ACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGT

          IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal
4081 ACATATTGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTG
     TGTATAACCCCCCCACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAAC

          GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp
4141 TGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAG
     ACCCGCGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATC

          IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer
4201 ACATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGA
     TGTAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACT

          GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly
4261 GCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCG
     CGCCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGC

          AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu
4321 GAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCG
     CTCGGGAGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGC

          GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer
4381 AGGGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTT
     TCCCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAA

          ProThrHisTyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSer
4441 CCCCCACGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCA
     GGGGGTGCGTGATGCACGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGT

          LeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThr
4501 GCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCA
     CGGAGTGACATTGGGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGT

          ProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAsp
4561 CTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCG
     GAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGC

          PheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSer
4621 ACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGT
     TGAAATTCTGGACCGATTTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACA

          CysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMetHisThrArgCysHis
4681 CCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCC
     GGACGGTCGCGCCCATATTCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGG

          CysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArg
4741 ACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTA
     TGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGAT

          ThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCys
4801 GGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCT
     CCTGGACGTCCTTGTACACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGA

          ThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyr
4861 GTACCCCCCTTCCTGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAAT
     CATGGGGGGAAGGACGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTA

          ValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeu
4921 ATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATC
     TACACCTCTATTCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAG

          LysCysProCysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeu
4981 TCAAATGCCCGTGCCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCC
     AGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGG
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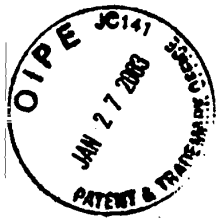

FIG. 47F

HisArgPheAlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGly
5041 TACATAGGTTTGCGCCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAG
ATGTATCCAAACGCGGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATC

LeuHisGluTyrProValGlySerGlnLeuProCysGluProGluProAspValAlaVal
5101 GACTCCACGAATACCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCG
CTGAGGTGCTTATGGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGC

LeuThrSerMetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeu
5161 TGTTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGT
ACAACTGCAGGTACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCA

AlaArgGlySerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSer
5221 TGGCGAGGGGATCACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCAT
ACCGCTCCCCTAGTGGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTA

LeuLysAlaThrCysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsn
5281 CTCTCAAGGCAACTTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCA
GAGAGTTCCGTTGAACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGT

LeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysVal
5341 ACCTCCTATGGAGGCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAG
TGGAGGATACCTCCGTCCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTC

ValIleLeuAspSerPheAspProLeuValAlaGluGluAspGluArgGluIleSerVal
5401 TGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCG
ACCACTAAGACCTGAGGAAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGC

ProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArg
5461 TACCCGCAGAAATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGC
ATGGGCGTCTTTAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCG

ProAspTyrAsnProProLeuValGluThrTrpLysLysProAspTyrGluProProVal
5521 GGCCGGACTATAACCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTG
CCGGCCTGATATTGGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGAC

ValHisGlyCysProLeuProProProLysSerProProValProProProArgLysLys
5581 TGGTCCATGGCTGTCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGA
ACCAGGTACCGACAGGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCT

ArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArg
5641 AGCGGACGGTGGTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCA
TCGCCTGCCACCAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGT

SerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGlu
5701 GAAGCTTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTG
CTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGAC

ProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProPro
5761 AGCCCGCCCCCTTCTGGCTGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCC
TCGGGCGGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGG

LeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSer
5821 CCCTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTA
GGGACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCAT

GluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeu
5881 GTGAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCAC
CACTCCGGTTGCGCCTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTG

ValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeu
5941 TCGTCACCCCGTGCGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGT
AGCAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCA

LeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLys
6001 TGCTACGTCACCACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGA
ACGATGCAGTGGTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCT

FIG. 47G

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                LysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGlu
6061 AGAAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGG
     TCTTTCAGTGTAAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCC

                ValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSer
6121 AGGTTAAAGCAGCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCA
     TCCAATTTCGTCGCCGCAGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGT

                LeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCys
6181 GCCTGACGCCCCCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTT
     CGGACTGCGGGGGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAA

                HisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsn
6241 GCCATGCCAGAAAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACA
     CGGTACGGTCTTTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGT

                ValThrProIleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGlu
6301 ATGTAACACCAATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTG
     TACATTGTGGTTATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGAC

                LysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCys
6361 AGAAGGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGT
     TCTTCCCCCCAGCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACA

                GluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSer
6421 GCGAAAAGATGGCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCT
     CGCTTTTCTACCGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGA

                TyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSer
6481 CCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGT
     GGATGCCTAAGGTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCA

                LysLysThrProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGlu
6541 CCAAGAAAACCCCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTG
     GGTTCTTTTGGGGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGAC

                SerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArg
6601 AGAGCGACATCCGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCC
     TCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGG

                ValAlaIleLysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArg
6661 GCGTGGCCATCAAGTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAA
     CGCACCGGTAGTTCAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTT

                GlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGly
6721 GGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTG
     CCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACAC

                AsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAsp
6781 GTAACACCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGG
     CATTGTGGGAGTGAACGATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCC

                CysThrMetLeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGln
6841 ACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCC
     TGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGG

                GluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProPro
6901 AGGAGGACGCGGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCC
     TCCTCCTGCGCCGCTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGG

                GlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnVal
6961 CTGGGGACCCCCCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACG
     GACCCCTGGGGGGTGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGC

                SerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThr
7021 TGTCAGTCGCCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAA
     ACAGTCAGCGGGTGCTGCCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTT
```

FIG. 47H

```
      ProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGly
7081  CCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAG
      GGGGGGAGCGCTCTCGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATC

      AsnIleIleMetPheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePhe
7141  GCAACATAATCATGTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCT
      CGTTGTATTAGTACAAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGA

      SerValLeuIleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAla
7201  TTAGCGTCCTTATAGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGG
      AATCGCAGGAATATCGGTCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCC

      CysTyrSerIleGluProLeuAspLeuProProIleIleGlnArgLeu
7261  CCTGCTACTCCATAGAACCACTTGATCTACCTCCAATCATTCAAAGACTC
      GGACGATGAGGTATCTTGGTGAACTAGATGGAGGTTAGTAAGTTTCTGAG
```

FIG. 48

```
     ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly
   1 CTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGCGCGCCTACCTACAGCTGGG
     GAGGGTCGGGGCACCACCACCCTTGCTGGCTGTCCAGCCCGCGCGGATGGATGTCGACCC
     GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe
  61 GTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGT
     CACTTTTACTATGCCTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCA
     GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal
 121 TCGGTTGTACCTGGATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGCCTCCTTGTG
     AGCCAACATGGACCTACTTGAGTTGACCTAAGTGGTTTCACACGCCTCGCGGAGGAACAC
     IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro
 181 TCATCGGAGGGGCGGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCCGCAAGCATC
     AGTAGCCTCCCCGCCCGTTGTTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCGTAG
     AspAlaThrTyrSerArgCysGlySerGlyProTrpLeuThrProArgCysLeuValAsp
 241 CGGACGCCACATACTCTCGGTGCGGCTCCGGTCCCTGGCTCACACCCAGGTGCCTGGTCG
     GCCTGCGGTGTATGAGAGCCACGCCGAGGCCAGGGACCGAGTGTGGGTCCACGGACCAGC
                                                   ---------------
     TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg
 301 ACTACCCGTATAGGCTTTGGCATTATCCTTGTACCATCAACTACACCATATTTAAAATCA
     TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTTAGT
     ------------------------------------------------------------
     MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu
 361 GGATGTACGTGGGAGGGGTCGAGCACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCG
     CCTACATGCACCCTCCCCAGCTCGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGC
     ---------------Overlap with 12f-----------------------------
     ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr
 421 AACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA
     TTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGAT
     ------------------------------------------------------------
     GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeu
 481 CACAGTGGCAGGTCCTCCCGTGTTCCTTCACAACCCTGCCAGCCTTGTCCACCGGCCTCA
     GTGTCACCGTCCAGGAGGGCACAAGGAAGTGTTGGGACGGTCGGAACAGGTGGCCGGAGT
```

FIG. 49

```
     LeuPheTyrHisHisLysPheAsnSerSerGlyCysProGluArgLeuAlaSerCysArg
   1 GCTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCCTGAGAGGCTAGCCAGCTGCCG
     CGAAAAGATAGTGGTGTTCAAGTTGAGAAGTCCGACAGGACTCTCCGATCGGTCGACGGC

     ProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGlyPro
  61 ACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCC
     TGGGGAATGGCTAAAACTGGTCCCGACCCCGGGATAGTCAATACGGTTGCCTTCGCCGGG

     AspGlnArgProTyrCysTrpHisTyrProProLysProCysGlyIleValProAlaLys
 121 CGACCAGCGCCCCTACTGCTGGCACTACCCCCCAAAACCTTGCGGTATTGTGCCCGCGAA
     GCTGGTCGCGGGGATGACGACCGTGATGGGGGGTTTTGGAACGCCATAACACGGGCGCTT

                                        ---Overlap with 13i---
     SerValCysGlyProValTyrCysPheThrProSerProValValVal
 181 GAGTGTGTGTGGTCCGGTATATTGCTTCACTCCCAGCCCCGTGGTGGTGGG
     CTCACACACACCAGGCCATATAACGAAGTGAGGGTCGGGGCACCACCACCC
```

FIG. 50

```
   LeuValMetAlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIleAlaGlyAla
 1 TTGGTAATGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCT
   AACCATTACCGAGTCGACGAGGCCTAGGGTGTTCGGTAGAACCTGTACTAGCGACCACGA

   HisTrpGlyValLeuAlaGlyIleAlaTyrPheSerMetValGlyAsnTrpAlaLysVal
61 CACTGGGGAGTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTC
   GTGACCCCTCAGGACCGCCCGTATCGCATAAAGAGGTACCACCCCTTGACCCGCTTCCAG

   LeuValValLeuLeuLeuPheAlaGlyValAspAlaGluThrHisValThrGlyGlySer
121 CTGGTAGTGCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTCACCGGGGGAAGT
   GACCATCACGACGACGATAAACGGCCGCAGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCA

   AlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal
181 GCCGGCCACACTGTGTCTGGATTTGTTAGCCTCCTCGCACCAGGCGCCAAGCAGAACGTC
   CGGCCGGTGTGACACAGACCTAAACAATCGGAGGAGCGTGGTCCGCGGTTCGTCTTGCAG

   GlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsnCysAsnAsp
241 CAGCTGATCAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAACTGCAATGAT
   GTCGACTAGTTGTGGTTGCCGTCAACCGTGGAGTTATCGTGCCGGGACTTGACGTTACTA
                                                    -----

   SerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsnSerSerGly
301 AGCCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGC
   TCGGAGTTGTGGCCGACCAACCGTCCCGAAAAGATAGTGGTGTTCAAGTTGAGAAGTCCG
                                 ------Overlap with 26j------------

   ------Overlap with K9-1--------
   CysProGluArgLeuAlaSerCysArgPro
361 TGTCCTGAGAGGCTAGCCAGCTGCCGACCCC
   ACAGGACTCTCCGATCGGTCGACGGCTGGGG
   --------------------------------
```

FIG. 51

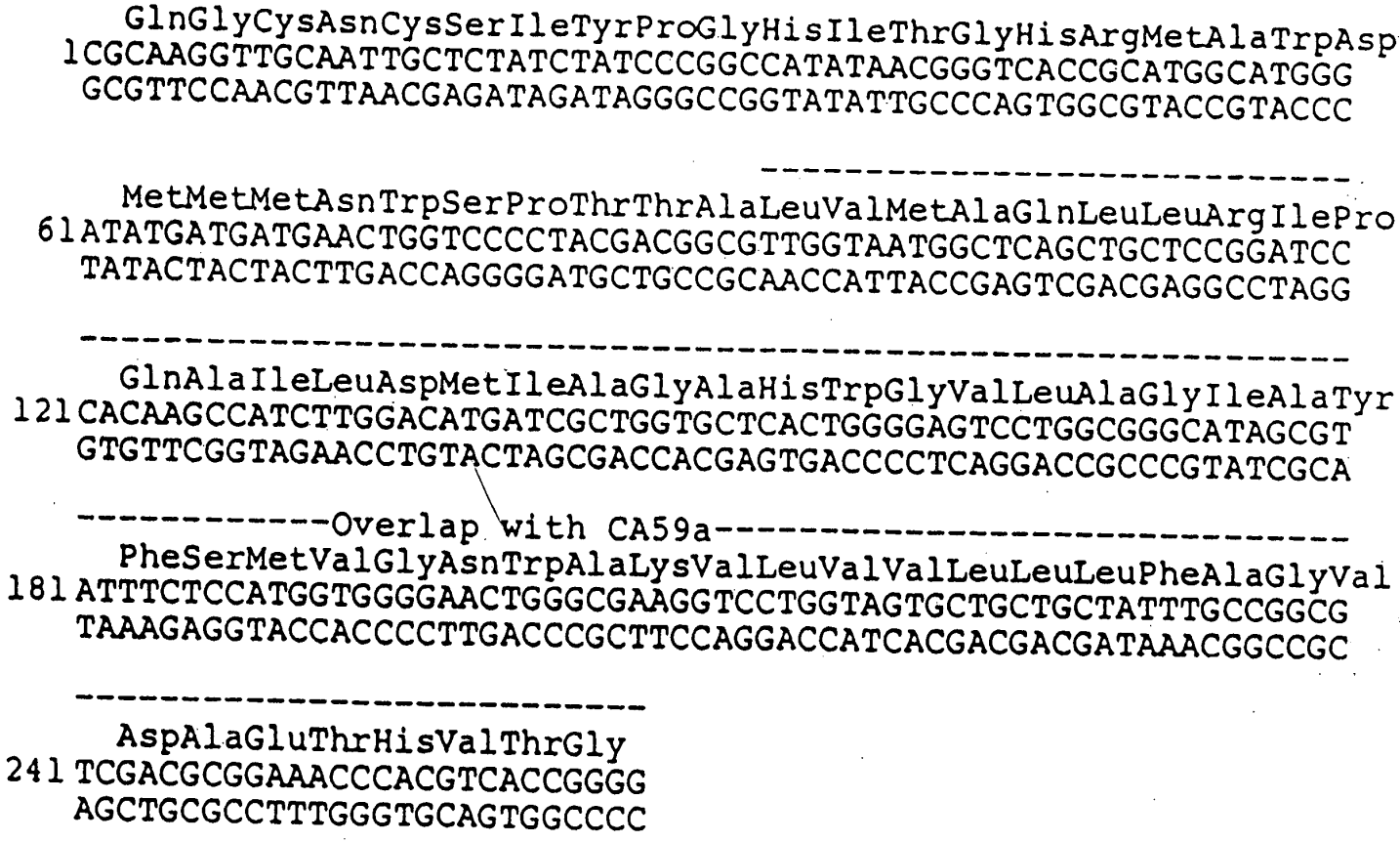

FIG. 52

```
     CysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThrGln
   1 GTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCCCGCGACGCA
     CACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGGGCGCTGCGT

     LeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCysSerAlaLeuTyrVal
  61 GCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTTCGGCCCTCTACGT
     CGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAGCCGGGAGATGCA

     GlyAspLeuCysGlySerValPheLeuValGlyGlnLeuPheThrPheSerProArgArg
 121 GGGGGACCTATGCGGGTCTGTCTTTCTTGTCGGCCAACTGTTCACCTTCTCTCCCAGGCG
     CCCCCTGGATACGCCCAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAGAGGGTCCGC

                 ------------------------------------------------

     HisTrpThrThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThrGlyHisArg
 181 CCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACGGGTCACCG
     GGTGACCTGCTGCGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTGCCCAGTGGC

     --------------------Overlap with CA84a----------------------
     MetAlaTrpAspMetMetMetAsnTrpSerProThrThrAlaLeuValValAlaGlnLeu
 241 CATGGCATGGGATATGATGATGAACTGGTCCCCTACGACGGCGTTGGTAGTGGCTCAGCT
     GTACCGTACCCTATACTACTACTTGACCAGGGGATGCTGCCGCAACCATCACCGAGTCGA

     --------------------
     LeuArgIleProGlnAla
 301 GCTCCGGATCCCACAAGCC
     CGAGGCCTAGGGTGTTCGG
```

FIG. 53

```
   SerThrGlyLeuTyrHisValThrAsnAspCysProAsnSerSerIleValTyrGluAla
 1 CTCCACGGGGCTTTACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTACGAGGC
   GAGGTGCCCCGAAATGGTGCAGTGGTTACTAACGGGATTGAGCTCATAACACATGCTCCG

   AlaAspAlaIleLeuHisThrProGlyCysValProCysValArgGluGlyAsnAlaSer
61 GGCCGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCAACGCCTC
   CCGGCTACGGTAGGACGTGTGAGGCCCCACGCAGGGAACGCAAGCACTCCCGTTGCGGAG

   ------------------------------------------------------------
   ArgCysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThr
121 GAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCCCGCGAC
   CTCCACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGGGCGCTG

   ------------------Overlap with CA156e-----------------------
   GlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCysSerAlaLeuTyr
181 GCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCTACCCTCTGTTCGGCCCTCTA
   CGTCGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGATGGGAGACAAGCCGGGAGAT

   --------------------------------
   ValGlyAspLeuCysGlySerValPheLeu
241 CGTGGGGGACTTGTGCGGGTCTGTCTTTCTTG
   GCACCCCCTGAACACGCCCAGACAGAAAGAAC
```

FIG. 54A

```
                ArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGlyPheAlaAspLeuMet
    1 AGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATG
      TCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGCCGAAGCGGCTGGAGTAC

                GlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAlaHisGly
   61 GGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGC
      CCCATGTATGGCGAGCAGCCGCGGGGAGAACCTCCGCGACGGTCCCGGGACCGCGTACCG

                ValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPhe
  121 GTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTTC
      CAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCTTGGAAGGACCAACGAGAAAG

                SerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValProAlaSerAlaTyrGlnVal
  181 TCTATCTTCCTTCTGGCCCTGCTCTCTTGCTTGACTGTGCCCGCTTCGGCCTACCAAGTG
      AGATAGAAGGAAGACCGGGACGAGAGAACGAACTGACACGGGCGAAGCCGGATGGTTCAC

                ArgAsnSerThrGlyLeuTyrHisValThrAsnAspCysProAsnSerSerIleValTyr
  241 CGCAACTCCACGGGGCTTTACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTAC
      GCGTTGAGGTGCCCCGAAATGGTGCAGTGGTTACTAACGGGATTGAGCTCATAACACATG

                GluAlaAlaAspAlaIleLeuHisThrProGlyCysValProCysValArgGluGlyAsn
  301 GAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCAAC
      CTCCGCCGGCTACGGTAGGACGTGTGAGGCCCCACGCAGGGAACGCAAGCACTCCCGTTG

                AlaSerArgCysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuPro
  361 GCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCCC
      CGGAGCTCCACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGGG

                AlaThrGlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCysSerAla
  421 GCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTTCGGCC
      CGCTGCGTCGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAGCCGG

                LeuTyrValGlyAspLeuCysGlySerValPheLeuValGlyGlnLeuPheThrPheSer
  481 CTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTCGGCCAACTGTTCACCTTCTCT
      GAGATGCACCCCCTGGATACGCCCAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAGA

                ProArgArgHisTrpThrThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThr
  541 CCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACG
      GGGTCCGCGGTGACCTGCTCCGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTGC

                GlyHisArgMetAlaTrpAspMetMetMetAsnTrpSerProThrThrAlaLeuValMet
  601 GGTCACCGCATGGCATGGGATATGATGATGAACTGGTCCCCTACGACGGCGTTGGTAATG
      CCAGTGGCGTACCGTACCCTATACTACTACTTGACCAGGGGATGCTGCCGCAACCATTAC
```

FIG. 54B

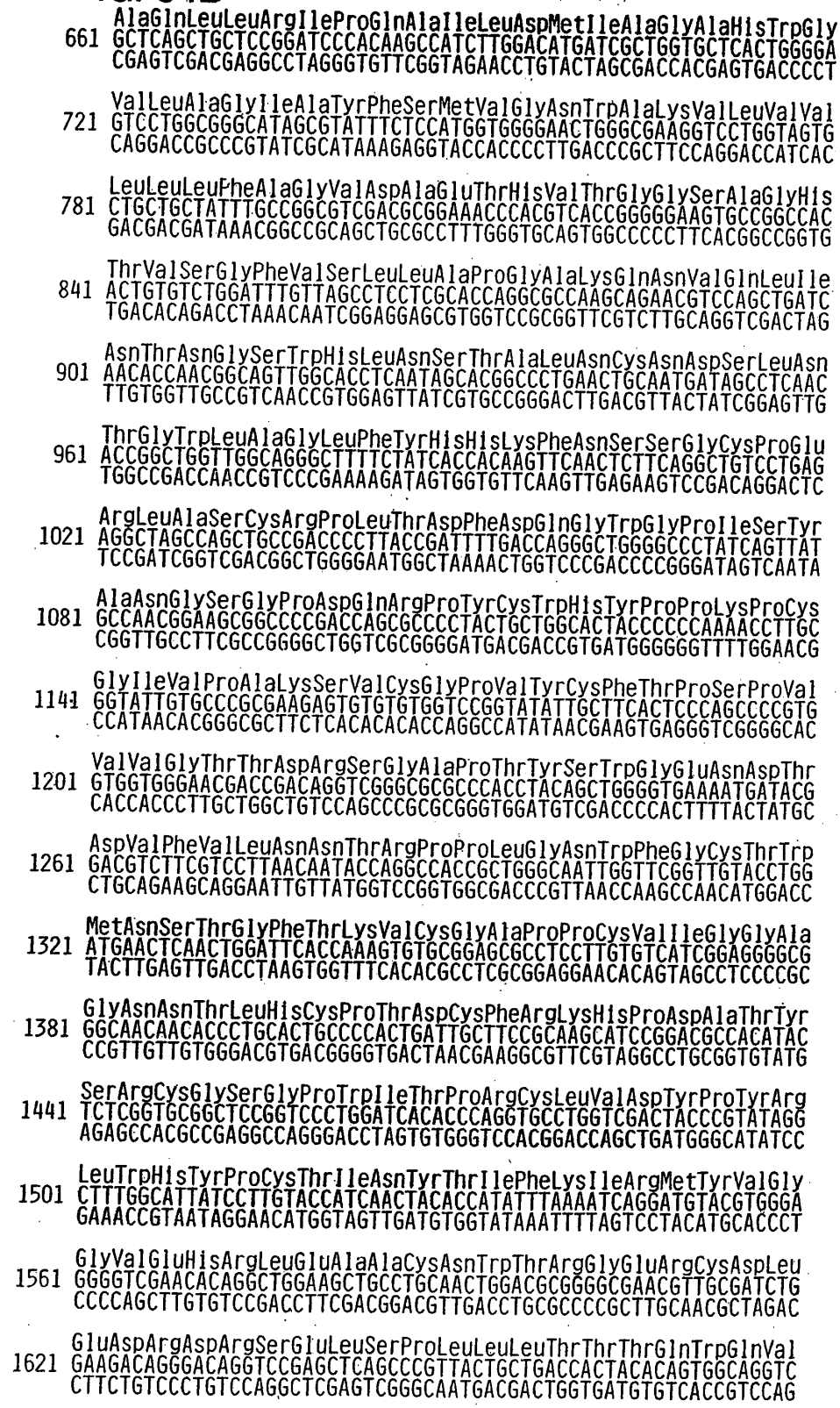

FIG. 54C

```
                LeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIleHisLeuHisGln
1681  CTCCCGTGTTCCTTCACAACCCTACCAGCCTTGTCCACCGGCCTCATCCACCTCCACCAG
      GAGGGCACAAGGAAGTGTTGGGATGGTCGGAACAGGTGGCCGGAGTAGGTGGAGGTGGTC

                AsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAlaSerTrpAlaIle
1741  AACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCGCGTCCTGGGCCATT
      TTGTAACACCTGCACGTCATGAACATGCCCCACCCCAGTTCGTAGCGCAGGACCCGGTAA

                LysTrpGluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCys
1801  AAGTGGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTGCAGACGCGCGCGTCTGCTCCTGC
      TTCACCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGACG

                LeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeu
1861  TTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTT
      AACACCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCTTGGAGCATTATGAA

                AsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPhe
1921  AATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCGTGTTCTTCTGCTTT
      TTACGTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAAA

                AlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrp
1981  GCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTGG
      CGTACCATAAACTTCCCATTCACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACC

                ProLeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluVal
2041  CCTCTCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGTG
      GGAGAGGAGGACGAGGACAACCGCAACGGGGTCGCCCGCATGCGCGACCTGTGCCTCCAC

                AlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyr
2101  GCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATAT
      CGGCGCAGCACACCGCCACAACAAGAGCAGCCCAACTACCGCGACTGAGACAGTGGTATA

                TyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGlu
2161  TACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGAA
      ATGTTCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTT

                AlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIle
2221  GCGCAACTGCACGTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCATC
      CGCGTTGACGTGCACACCTAAGGGGGGGAGTTGCAGGCTCCCCCCGCGCTGCGGCAGTAG

                LeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAla
2281  TTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCC
      AATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGTTTAACGACGACCGG

                ValPheGlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArg
2341  GTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGC
      CAGAAGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTCATGGGATGAAACACGCG

                ValGlnGlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrVal
2401  GTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTG
      CAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCAC

                GlnMetValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThr
2461  CAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACT
      GTTTACCAGTAGTAATTCAATCCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTGA

                ProLeuArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProVal
2521  CCTCTTCGGGACTGGGCGCACAACCGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTC
      GGAGAAGCCCTGACCCGCGTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAG

                ValPheSerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGly
2581  GTCTTCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGGT
      CAGAAGAGGGTTTACCTCTGGTTCGAGTAGTGCACCCCCCGTCTATGGCGGCGCACGCCA

                AspIleIleAsnGlyLeuProValSerAlaArgArgGlyArgGluIleLeuLeuGlyPro
2641  GACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCCA
      CTGTAGTAGTTGCCGAACGGACAAAGGCGGGCGTCCCCGGCCCTCTATGACGAGCCCGGT
```

FIG. 54D

```
                AlaAspGlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGln
2701            GCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCAG
                CGGCTACCTTACCAGAGGTTCCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGTC

                GlnThrArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGln
2761            CAGACAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCAA
                GTCTGTTCCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTTGGTT

                ValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIle
2821            GTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCATC
                CACCTCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAGGACCGTTGCACGTAG

                AsnGlyValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLys
2881            AATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAAG
                TTACCCCACACGACCTGACAGATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGGTTC

                GlyProValIelGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpProAlaPro
2941            GGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCG
                CCAGGACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGC

                GlnGlySerArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuValThr
3001            CAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACG
                GTTCCATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCAGTGC

                ArgHisAlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLeuSer
3061            AGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTCG
                TCCGTGCGGCTACAGTAAGGGCACGCGGCCGCCCCACTATCGTCCCCGTCGGACGACAGC

                ProArgProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGly
3121            CCCCGGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGGG
                GGGGCCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCCAGGCGACAACACGGGGCGCCCC

                HisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAsp
3181            CACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGAC
                GTGCGGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTCACCGATTCCGCCACCTG

                PheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThrAspAsnSer
3241            TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTCC
                AAATAGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAGG

                SerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaProThrGlySer
3301            TCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAGC
                AGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTCG

                GlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeu
3361            GGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTC
                CCGTTTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAG

                AsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIle
3421            AACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATC
                TTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAG

                AspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSer
3481            GATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCC
                CTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGG

                ThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIle
3541            ACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATT
                TGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAA

                CysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAsp
3601            TGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGAC
                ACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACTG
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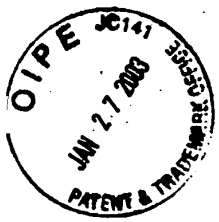


FIG. 54E

```
      GlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySer
3661  CAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCC
      GTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGG

      ValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIlePro
3721  GTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCT
      CAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGA

      PheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCys
3781  TTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGT
      AAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACA

      HisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAla
3841  CATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCC
      GTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGG

      ValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValVal
3901  GTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTC
      CACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAG

      ValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCys
3961  GTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGC
      CACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACG

      AsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThr
4021  AATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACA
      TTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGT

      IleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGly
4081  ATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGG
      TAGTGCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCC

      LysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSer
4141  AAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCG
      TTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGC

      SerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGlu
4201  TCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAG
      AGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTC

      ThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHis
4261  ACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCAT
      TGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTA

      LeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSer
4321  CTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCC
      GAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGG

      GlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCys
4381  CAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGC
      GTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACG

      AlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeu
4441  GCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTC
      CGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAG

      LysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGlu
4501  AAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAA
      TTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTT

      IleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGlu
4561  ATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAG
      TAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTC

      ValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCys
4621  GTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGC
      CAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACG
```

FIG. 54F

```
                LeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIle
4681 CTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATC
     GACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAG

                IleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHis
4741 ATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCAC
     TATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTG

                LeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGly
4801 TTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGC
     AATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCG

                LeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAspTrp
4861 CTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGG
     GAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACC

                GlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyr
4921 CAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATAC
     GTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATG

                LeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThr
4981 TTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACA
     AACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGT

                AlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGly
5041 GCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGG
     CGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCC

                TrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeu
5101 TGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTA
     ACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAAT

                AlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGly
5161 GCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGG
     CGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCC

                TyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValPro
5221 TATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCC
     ATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGG

                SerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValVal
5281 TCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTC
     AGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAG

                GlyValValCysAlaAlaIleLeuArgARgHisValGlyProGlyGluGlyAlaValGln
5341 GGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAG
     CCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTC

                TrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyr
5401 TGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTAC
     ACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATG

                ValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThr
5461 GTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACC
     CACGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGG

                GlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGly
5521 CAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGT
     GTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCA

                SerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrp
5581 TCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGG
     AGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACC

                LeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGly
5641 CTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGG
     GATTTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCC
```

FIG. 54G

```
                TyrLysGlyValTrpArgValAspGlyIleMetHisThrArgCysHisCysGlyAlaGlu
5701  TATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAG
      ATATTCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTC

                IleThrGlyHisValLysAsnGlyThrMetArgIleValGlyPRoArgThrCysArgAsn
5761  ATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAAC
      TAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTG

                MetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuPro
5821  ATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCT
      TACACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGA

                AlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArg
5881  GCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAGG
      CGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATACACCTCTATTCC

                GlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCys
5941  CAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTGC
      GTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAGTTTACGGGCACG

                GlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAla
6001  CAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCG
      GTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGC

                ProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyr
6061  CCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATAC
      GGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATG

                ProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMet
6121  CCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATG
      GGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTAC

                LeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySer
6181  CTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCA
      GAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGT

                ProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThr
6241  CCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACT
      GGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGA

                CysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArg
6301  TGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGG
      ACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCC

                GlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAsp
6361  CAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGAC
      GTCCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTG

                SerPheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIle
6421  TCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATC
      AGGAAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAG

                LeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsn
6481  CTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAAC
      GACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTG

                ProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCys
6541  CCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGT
      GGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACA

                ProLeuProProProLysSerProProValProProProArgLysLysArgThrValVal
6601  CCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTC
      GGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAG

                LeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySer
6661  CTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGC
      GAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCG
```

FIG. 54H

```
                SerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSer
6721 TCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCT
     AGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGA

                GlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGlu
6781 GGCTGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAG
     CCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTC

                ProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAla
6841 CCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCG
     GGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGC

                GluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCys
6901 GAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGC
     CTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACG

                AlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHis
6961 GCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCAC
     CGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTG

                AsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPhe
7021 AATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTT
     TTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAA

                AspARgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAla
7081 GACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCG
     CTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGC

                AlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProPro
7141 GCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCA
     CGCAGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGT

                HisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLys
7201 CACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAG
     GTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTC

                AlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIle
7261 GCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATA
     CGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTAT

                AspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArg
7321 GACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGT
     CTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCA

                LysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAla
7381 AAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCT
     TTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGA

                LeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGln
7441 TTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAA
     AACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTT

                TyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrPro
7501 TACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCA
     ATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGT

                MetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArg
7561 ATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGT
     TACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCA

                ThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLys
7621 ACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAG
     TGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTC

                SerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCys
7681 TCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGC
     AGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACG
```

FIG. 54I

```
     GlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThr
7741 GGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACT
     CCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGA

     CysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeu
7801 TGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTC
     ACGATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAG

     ValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAla
7861 GTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCG
     CACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGC

     SerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProPro
7921 AGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCA
     TCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGGACCCCTGGGGGGT

     GlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHis
7981 CAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCAC
     GTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTG

     AspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArg
8041 GACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGA
     CTGCCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCT

     AlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMet
8101 GCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATG
     CGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTAC

     PheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIle
8161 TTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATA
     AAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATAT

     AlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIle
8221 GCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATA
     CGGTCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTAT

     GluProLeuAspLeuProProIleIleGlnArgLeu
8281 GAACCACTTGATCTACCTCCAATCATTCAAAGACTC
     CTTGGTGAACTAGATGGAGGTTAGTAAGTTTCTGAG
```

FIG. 55A

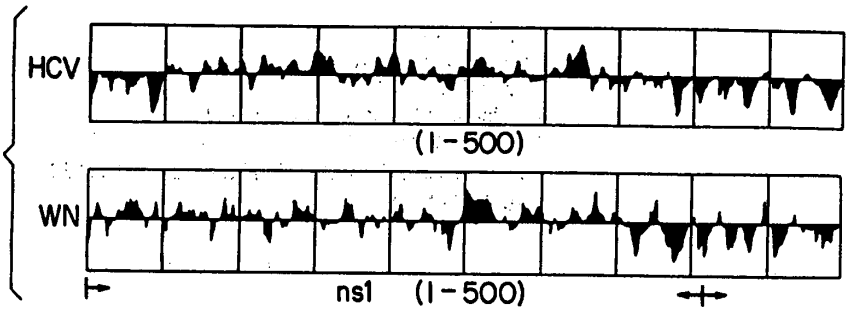


FIG. 55B

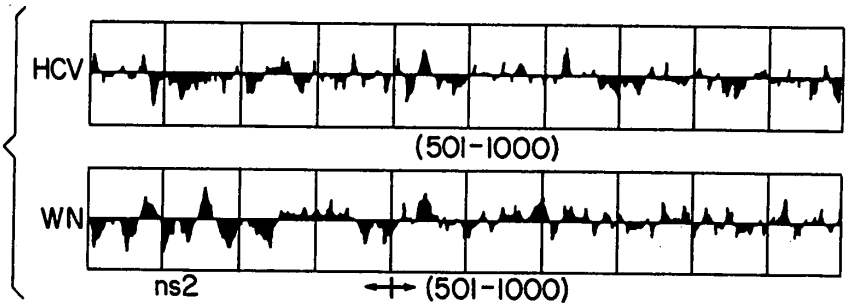


FIG. 55C

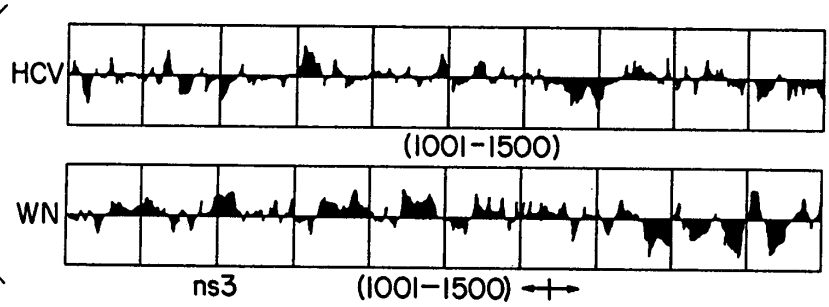


FIG. 55D

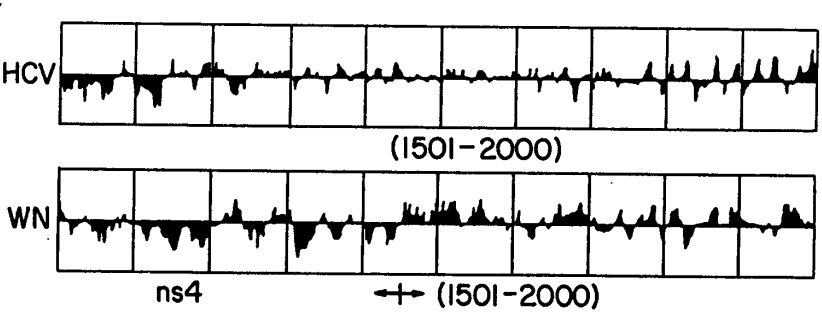


FIG. 55E

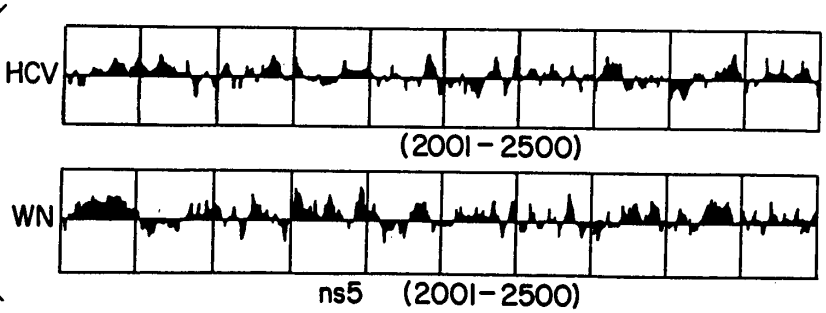
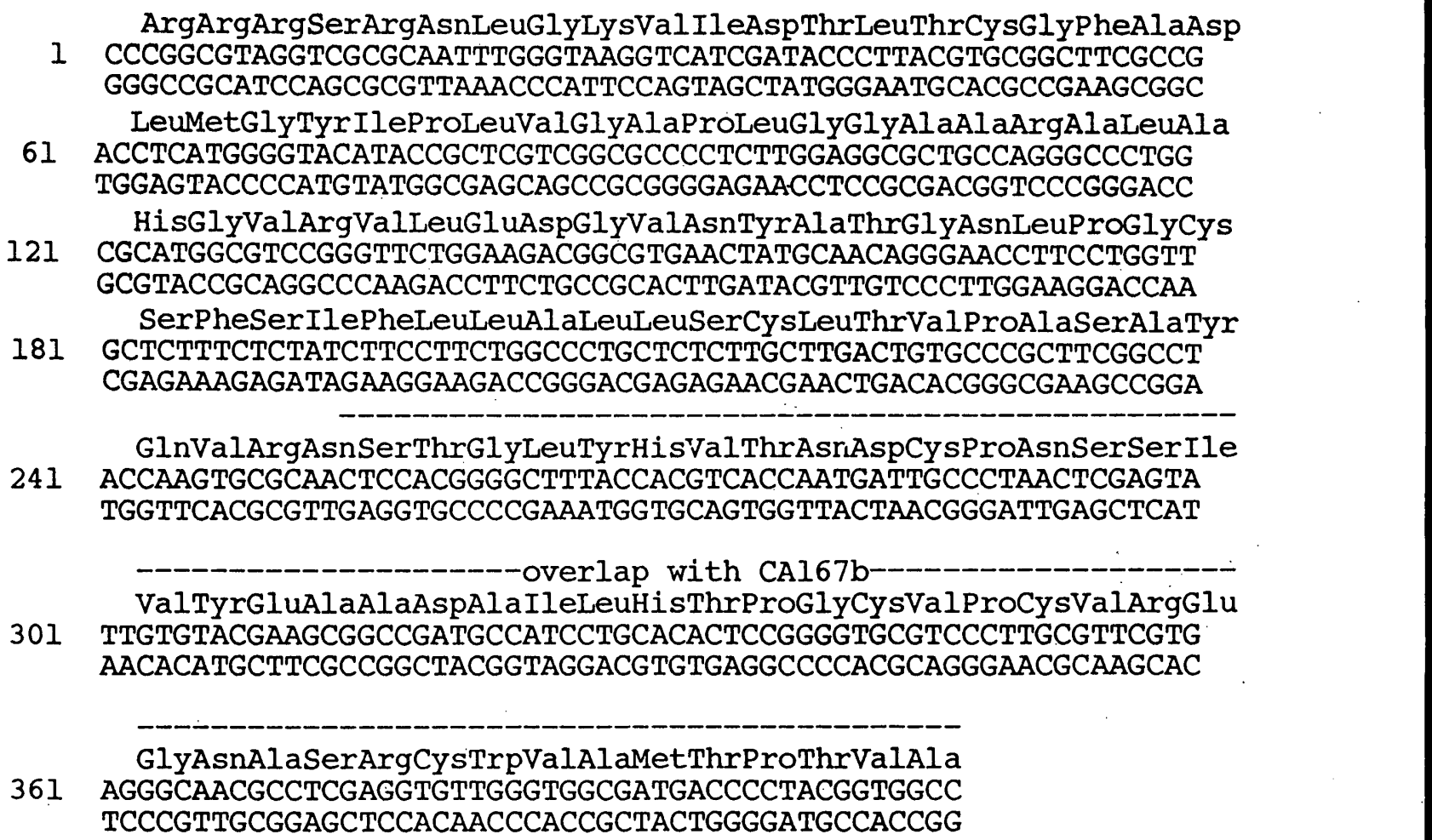


FIG. 56



```
      LysLysAsnLysArgAsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGly
1     AAAAAAAAAACAAACGTAACACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCG
      TTTTTTTTTTGTTTGCATTGTGGTTGGCAGCGGGTGTCCTGCAGTTCAAGGGCCCACCGC
      GlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAla
61    GTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCG
      CAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAACCCACACGCGC
      ThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnProIleProLysAla
121   CGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGCCAGCCTATCCCCAAGG
      GCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCGGTCGGATAGGGGTTCC
      ArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpProLeuTyrGlyAsn
181   CTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCA
      GAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGGGAGATACCGT
      GluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArgProSerTrpGly
241   ATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGG
      TACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCCGGATCGACCC
            ------------------------------------------------------
      ProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCys
301   GCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGT
      CGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCA
      ------------------------------------------------------------
      GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAla
361   GCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTG
      CGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAACCTCCGCGAC
      ------------------------overlap with CA216a------------------
      ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn
421   CCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGGA
      GGTCCCGGGACCGCGTACCGCAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCT
      ----------------------------
      LeuProGlyCysSerPheSerThrPhe
481   ACCTTCCTGGTTGCTCTTTCTCTACCTTC
      TGGAAGGACCAACGAGAAAGAGATGGAAG
```

FIG. 57

FIG. 58A

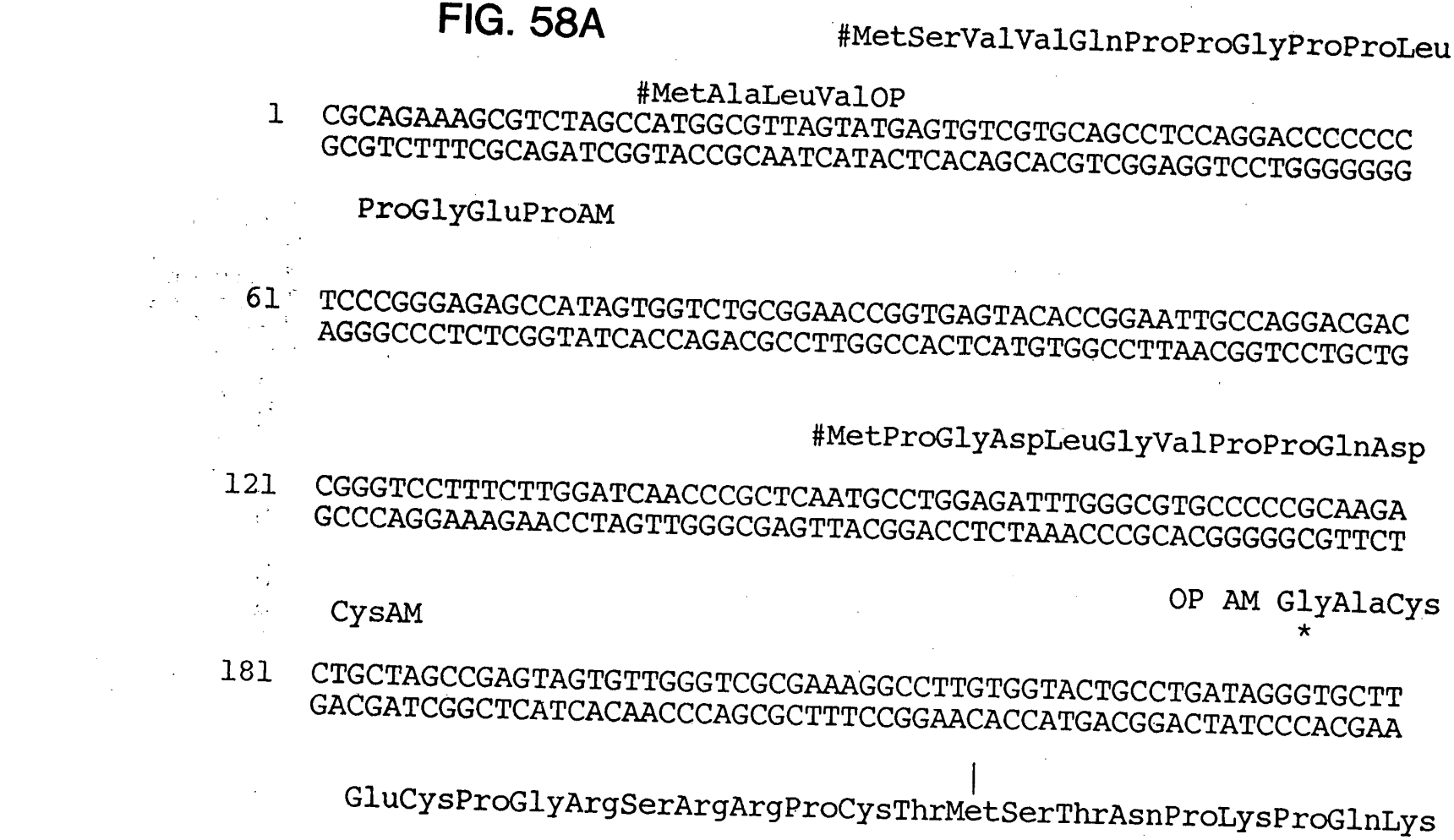


FIG. 58B

```
241  GCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAA
     CGCTCACGGGGCCCTCCAGAGCATCTGGCACGTGGTACTCGTGCTTAGGATTTGGAGTTT

       LysAsnLysArgAsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGlyGln

     ------------------------------------------------------------
301  AAAAAAACAAACGTAACACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTC
     TTTTTTTGTTTGCATTGTGGTTGGCAGCGGGTGTCCTGCAGTTCAAGGGCCCACCGCCAG

       IleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAlaThr

     ------------------------------------------------------------
361  AGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGA
     TCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAACCCACACGCGCGCT

       ArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArg

     ------------------------------------------------------------
421  CGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCTC
     GCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGATAGGGGTTCCGAG

       ArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpProLeuTyrGlyAsnGlu
```

```
          ------------------------overlap with CA290a-----------------
481       GTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATG
          CAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGGGAGATACCGTTAC

            GlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArgProSerTrpGlyPro

          ------------------------------------------------------------
541       AGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCC
          TCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCCGGATCGACCCCGG

            ThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGly
          ------------------------------------------------------------
601       CCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGCG
          GGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGC

            Phe

          -----
661       GCTTC
          CGAAG
```

* = Start of long HCV ORF
| = Putative first amino acid of large HCV polyprotein
= Putative small encoded peptides (that may play a translational regulatory role)

FIG. 58C

FIG. 59

```
    ValLeuGlyArgGluArgProCysGlyThrAlaOP AM GlyAlaCysGluCysProGly
  1 GTCTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGG
    CAGAACCCAGCGCTTTCCGGAACACCATGACGGACTATCCCACGAACGCTCACGGGGCCC

                                 *                 ----------------
    ArgSerArgArgProCysThrMetSerThrAsnProLysProGlnArgLysThrLysArg
 61 AGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGT
    TCCAGAGCATCTGGCACGTGGTACTCGTGCTTAGGATTTGGAGTTTCTTTTTGGTTTGCA

    ----------------------------------------------------------
    AsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleValGlyGly
121 AACACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGA
    TTGTGGTTGGCAGCGGGTGTCCTGCAGTTCAAGGGCCCACCGCCAGTCTAGCAACCACCT

    ----------------------------------------------------------
    ValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAlaThrArgLysThrSer
181 GTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCC
    CAAATGAACAACGGCGCGTCCCCGGGATCTAACCCACACGCGCGCTGCTCTTTCTGAAGG

    --------------------overlap with CA290a----------------------
    GluArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArgArgProGluGly
241 GAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCTCGTCGGCCCGAGGGC
    CTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGATAGGGGTTCCGAGCAGCCGGGCTCCCG

    ----------------------------------------------------------
    ArgThrTrpAlaGlnProGlyTyrProTrpProLeuTyrGlyAsnGluGlyCys
301 AGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCTGCG
    TCCTGGACCCGAGTCGGGCCCATGGGAACCGGGGAGATACCGTTACTCCCGACGC
          * = putative initiator methionine codon
```

FIG. 60

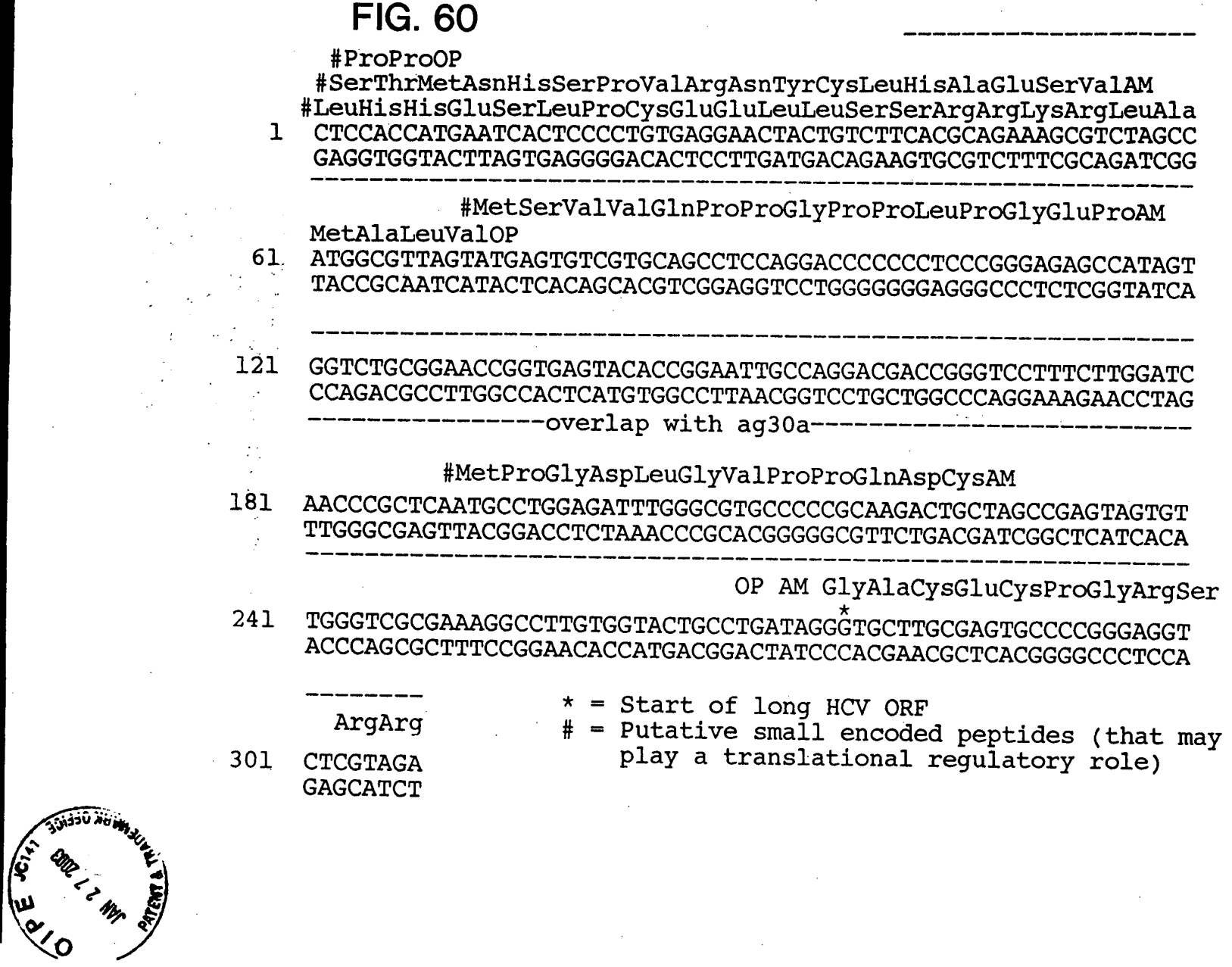


FIG. 61

* = nucleotide heterogeneity

FIG. 62A

```
                                                                  ------
CACTCCACCATGAATCACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAG
CCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCTCCCGGGAGAGCCATA
GTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGA
TCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGT
GTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAG-300

                        ---(Putative initiator methionine codon)
GTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAAAAAAAACAAACGTAA
CACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGT
TTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCCGA
GCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCTCGTCGGCCCGAGGGCAG
GACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGC-600
GGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCG
TAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCAT
GGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGG
CGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTT
CTCTATCTTCCTTCTGGCCCTGCTCTCTTGCTTGACTGTGCCCGCTTCGGCCTACCAAGT-900
GCGCAACTCCACGGGGCTTTACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTA
CGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCAA
CGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCC
CGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTTCGGC
CCTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTCGGCCAACTGTTCACCTTCTC-1200
TCCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAAC
GGGTCACCGCATGGCATGGGATATGATGATGAACTGGTCCCCTACGACGGCGTTGGTAAT
GGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
AGTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGT
GCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTCACCGGGGGAAGTGCCGGCCA-1500
CACTGTGTCTGGATTTGTTAGCCTCCTCGCACCAGGCGCCAAGCAGAACGTCCAGCTGAT
CAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAACTGCAATGATAGCCTCAA
CACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCCTGA
GAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTA
TGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCTGGCACTACCCCCCAAAACCTTG-1800
CGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCCAGCCCCGT
GGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCTACAGCTGGGGTGAAAATGATAC
GGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGTTCGGTTGTACCTG
GATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGCCTCCTTGTGTCATCGGAGGGGC
GGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCCGCAAGCATCCGGACGCCACATA-2100
CTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCGACTACCCGTATAG
GCTTTGGCATTATCCTTGTACCATCAACTACACCATATTTAAAATCAGGATGTACGTGGG
AGGGGTCGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCT
GGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTACACAGTGGCAGGT
CCTCCCGTGTTCCTTCACAACCCTACCAGCCTTGTCCACCGGCCTCATCCACCTCCACCA-2400
GAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCGCGTCCTGGGCCAT
TAACTGGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTGCAGACGCGCGCGTCTGCTCCTG
CTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACT
TAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCGTGTTCTTCTGCTT
TGCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTG-2700
GCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGT
GGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATA
TTACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGA
AGCGCAACTGCACGTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCAT
CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGC-3000
CGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCG
CGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGT
GCAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC
TCCTCTTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGT
CGTCTTCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGG-3300
TGACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCC
AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA
GCAGACAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA
AGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCAT
```

FIG. 62B

CAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAA-3600
GGGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCC
GCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCAC
GAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTC
GCCCCGGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGG
GCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGA-3900
CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTC
CTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAG
CGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT
CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGAT
CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTC-4200
CACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAAT
TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGA
CCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC
CGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC
TTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTG-4500
TCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGC
CGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGT
CGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTG
CAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGAC
AATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGG-4800
GAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTC
GTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGA
GACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCA
TCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATC
CCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTG-5100
CGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCT
CAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGA
AATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGA
GGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTG
CCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAAT-5400
CATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCA
CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG
CCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTG
GCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATA
CTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC-5700
AGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGG
GTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTT
AGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGG
GTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCC
CTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGT-6000
CGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCA
GTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTA
CGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAAC
CCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGG
TTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG-6300

FIG. 62C

GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGG
GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA
GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAA
CATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCC
TGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG-6600
GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG
CCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGC
GCCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATA
CCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCAT
GCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATC-6900
ACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC
TTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG
GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGA
CTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAAT
CCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAA-7200
CCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTG
TCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGT
CCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAG
CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTC
TGGCTGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGA-7500
GCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGC
GGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTG
CGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCA
CAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATT
TGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGC-7800
GGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCC
ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA
GGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAAT
AGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCG
TAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGC-8100
TTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCA
ATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCC
AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG
TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAA
GTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTG-8400
CGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCAC
TTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCT
CGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGC
GAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCC
ACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCA-8700
CGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAG
AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT
GTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTAT
AGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCAT
AGAACCACTTGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACT-9000
CCACAGTTACTCTCCAGGTGAAATTAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGT
ACCGCCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAG
AGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCT
CAAAC

FIG. 62D

```
   1 CACTCCACCATGAATCACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAG
     GTGAGGTGGTACTTAGTGAGGGGACACTCCTTGATGACAGAAGTGCGTCTTTCGCAGATC

  61 CCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCTCCCGGGAGAGCCATA
     GGTACCGCAATCATACTCACAGCACGTCGGAGGTCCTGGGGGGGAGGGCCCTCTCGGTAT

 121 GTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGA
     CACCAGACGCCTTGGCCACTCATGTGGCCTTAACGGTCCTGCTGGCCCAGGAAAGAACCT

 181 TCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGT
     AGTTGGGCGAGTTACGGACCTCTAAACCCGCACGGGGGCGTTCTGACGATCGGCTCATCA

 241 GTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAG
     CAACCCAGCGCTTTCCGGAACACCATGACGGACTATCCCACGAACGCTCACGGGGCCCTC

 301 GTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAAAAAAAACAAACGTAA
     CAGAGCATCTGGCACGTGGTACTCGTGCTTAGGATTTGGAGTTTTTTTTTTGTTTGCATT

 361 CACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGT
     GTGGTTGGCAGCGGGTGTCCTGCAGTTCAAGGGCCCACCGCCAGTCTAGCAACCACCTCA

 421 TTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCCGA
     AATGAACAACGGCGCGTCCCCGGGATCTAACCCACACGCGCGCTGCTCTTTCTGAAGGCT

 481 GCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCTCGTCGGCCCGAGGGCAG
     CGCCAGCGTTGGAGCTCCATCTGCAGTCGGATAGGGGTTCCGAGCAGCCGGGCTCCCGTC

 541 GACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGC
     CTGGACCCGAGTCGGGCCCATGGGAACCGGGGAGATACCGTTACTCCCGACGCCCACCCG

 601 GGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCG
     CCCTACCGAGGACAGAGGGGCACCGAGAGCCGGATCGACCCCGGGGTGTCTGGGGGCCGC

 661 TAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCAT
     ATCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGCCGAAGCGGCTGGAGTA

 721 GGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGG
     CCCCATGTATGGCGAGCAGCCGCGGGGAGAACCTCCGCGACGGTCCCGGGACCGCGTACC

 781 CGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTT
     GCAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCTTGGAAGGACCAACGAGAAA

 841 CTCTATCTTCCTTCTGGCCCTGCTCTCTTGCTTGACTGTGCCCGCTTCGGCCTACCAAGT
     GAGATAGAAGGAAGACCGGGACGAGAGAACGAACTGACACGGGCGAAGCCGGATGGTTCA

 901 GCGCAACTCCACGGGGCTTTACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTA
     CGCGTTGAGGTGCCCCGAAATGGTGCAGTGGTTACTAACGGGATTGAGCTCATAACACAT

 961 CGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCAA
     GCTCCGCCGGCTACGGTAGGACGTGTGAGGCCCCACGCAGGGAACGCAAGCACTCCCGTT

1021 CGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCC
     GCGGAGCTCCACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGG

1081 CGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTTCGGC
     GCGCTGCGTCGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAGCCG

1141 CCTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTCGGCCAACTGTTCACCTTCTC
     GGAGATGCACCCCCTGGATACGCCCAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAG

1201 TCCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAAC
     AGGGTCCGCGGTGACCTGCTGCGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTG

1261 GGGTCACCGCATGGCATGGGATATGATGATGAACTGGTCCCCTACGACGGCGTTGGTAAT
     CCCAGTGGCGTACCGTACCCTATACTACTACTTGACCAGGGGATGCTGCCGCAACCATTA
```

FIG. 62E

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1321 GGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
     CCGAGTCGACGAGGCCTAGGGTGTTCGGTAGAACCTGTACTAGCGACCACGAGTGACCCC

1381 AGTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGT
     TCAGGACCGCCCGTATCGCATAAAGAGGTACCACCCCTTGACCCGCTTCCAGGACCATCA

1441 GCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTCACCGGGGGAAGTGCCGGCCA
     CGACGACGATAAACGGCCGCAGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCACGGCCGGT

1501 CACTGTGTCTGGATTTGTTAGCCTCCTCGCACCAGGCGCCAAGCAGAACGTCCAGCTGAT
     GTGACACAGACCTAAACAATCGGAGGAGCGTGGTCCGCGGTTCGTCTTGCAGGTCGACTA

1561 CAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAACTGCAATGATAGCCTCAA
     GTTGTGGTTGCCGTCAACCGTGGAGTTATCGTGCCGGGACTTGACGTTACTATCGGAGTT

1621 CACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCCTGA
     GTGGCCGACCAACCGTCCCGAAAAGATAGTGGTGTTCAAGTTGAGAAGTCCGACAGGACT

1681 GAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTA
     CTCCGATCGGTCGACGGCTGGGGAATGGCTAAAACTGGTCCCGACCCCGGGATAGTCAAT

1741 TGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCTGGCACTACCCCCCAAAACCTTG
     ACGGTTGCCTTCGCCGGGGCTGGTCGCGGGGATGACGACCGTGATGGGGGGTTTTGGAAC

1801 CGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCCAGCCCCGT
     GCCATAACACGGGCGCTTCTCACACACACCAGGCCATATAACGAAGTGAGGGTCGGGGCA

1861 GGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCTACAGCTGGGGTGAAAATGATAC
     CCACCACCCTTGCTGGCTGTCCAGCCCGCGCGGGTGGATGTCGACCCCACTTTTACTATG

1921 GGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGTTCGGTTGTACCTG
     CCTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCAAGCCAACATGGAC

1981 GATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGCCTCCTTGTGTCATCGGAGGGGC
     CTACTTGAGTTGACCTAAGTGGTTTCACACGCCTCGCGGAGGAACACAGTAGCCTCCCCG

2041 GGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCCGCAAGCATCCGGACGCCACATA
     CCCGTTGTTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCGTAGGCCTGCGGTGTAT

2101 CTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCGACTACCCGTATAG
     GAGAGCCACGCCGAGGCCAGGGACCTAGTGTGGGTCCACGGACCAGCTGATGGGCATATC

2161 GCTTTGGCATTATCCTTGTACCATCAACTACACCATATTTAAAATCAGGATGTACGTGGG
     CGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTTAGTCCTACATGCACCC

2221 AGGGGTCGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCT
     TCCCCAGCTTGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGCTTGCAACGCTAGA

2281 GGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTACACAGTGGCAGGT
     CCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGATGTGTCACCGTCCA

2341 CCTCCCGTGTTCCTTCACAACCCTACCAGCCTTGTCCACCGGCCTCATCCACCTCCACCA
     GGAGGGCACAAGGAAGTGTTGGGATGGTCGGAACAGGTGGCCGGAGTAGGTGGAGGTGGT

2401 GAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCGCGTCCTGGGCCAT
     CTTGTAACACCTGCACGTCATGAACATGCCCCACCCCAGTTCGTAGCGCAGGACCCGGTA

2461 TAAGTGGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTGCAGACGCGCGCGTCTGCTCCTG
     ATTCACCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGAC

2521 CTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACT
     GAACACCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCTTGGAGCATTATGA

2581 TAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCGTGTTCTTCTGCTT
     ATTACGTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAA
```

FIG. 62F

2641 TGCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTG
ACGTACCATAAACTTCCCATTCACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACAC

2701 GCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGT
CGGAGAGGAGGACGAGGACAACCGCAACGGGGTCGCCCGCATGCGCGACCTGTGCCTCCA

2761 GGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATA
CCGGCGCAGCACACCGCCACAACAAGAGCAGCCCAACTACCGCGACTGAGACAGTGGTAT

2821 TTACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGA
AATGTTCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCT

2881 AGCGCAACTGCACGTGTGGATTCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCAT
TCGCGTTGACGTGCACACCTAAGGGGGGGAGTTGCAGGCTCCCCCCGCGCTGCGGCAGTA

2941 CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGC
GAATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGTTTAACGACGACCG

3001 CGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCG
GCAGAAGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTCATGGGATGAAACACGC

3061 CGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGT
GCAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCA

3121 GCAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC
CGTTTACCAGTAGTAATTCAATCCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTG

3181 TCCTCTTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGT
AGGAGAAGCCCTGACCCGCGTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCA

3241 CGTCTTCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGG
GCAGAAGAGGGTTTACCTCTGGTTCGAGTAGTGCACCCCCCGTCTATGGCGGCGCACGCC

3301 TGACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCC
ACTGTAGTAGTTGCCGAACGGACAAAGGCGGGCGTCCCCGGCCCTCTATGACGAGCCCGG

3361 AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA
TCGGCTACCTTACCAGAGGTTCCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGT

3421 GCAGACAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA
CGTCTGTTCCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTTGGT

3481 AGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCAT
TCACCTCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAGGACCGTTGCACGTA

3541 CAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAA
GTTACCCCACACGACCTGACAGATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGGTT

3601 GGGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCC
CCCAGGACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGG

3661 GCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCAC
GCTTCCATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCAGTG

3721 GAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTC
CTCCGTGCGGCTACAGTAAGGGCACGCGGCCGCCCCACTATCGTCCCCGTCGGACGACAG

3781 GCCCCGGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGG
CGGGGCCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCCAGGCGACAACACGGGGCGCCC

3841 GCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGA
CGTGCGGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTCACCGATTCCGCCACCT

3901 CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTC
GAAATAGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAG

FIG. 62G

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3961 CTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAG
     GAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTC

4021 CGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT
     GCCGTTTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGA

4081 CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGAT
     GTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTA

4141 CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTC
     GCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAG

4201 CACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAAT
     GTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTA

4261 TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGA
     AACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACT

4321 CCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC
     GGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAG

4381 CGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC
     GCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGG

4441 TTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTG
     AAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGAC

4501 TCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGC
     AGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACG

4561 CGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGT
     GCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCA

4621 CGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTG
     GCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGAC

4681 CAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGAC
     GTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTG

4741 AATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGG
     TTAGTGCGAGGGGGTCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCC

4801 GAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTC
     CTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAG

4861 GTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGA
     CAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCT

4921 GACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCA
     CTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGT

4981 TCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATC
     AGAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAG

5041 CCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTG
     GGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACAC

5101 CGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCT
     GCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGA

5161 CAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGA
     GTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACT

5221 AATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGA
     TTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCT
```

FIG. 62H

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5281 GGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTG
     CCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAAC

5341 CCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAAT
     GGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTA

5401 CATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCA
     GTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGT

5461 CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG
     GAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCC

5521 CCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTG
     GGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGAC

5581 GCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATA
     CGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTAT

5641 CTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC
     GAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATG

5701 AGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGG
     TCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCC

5761 GTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTT
     CACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAA

5821 AGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGG
     TCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCC

5881 GTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCC
     CATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGG

5941 CTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGT
     GAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCA

6001 CGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCA
     GCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGT

6061 GTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTA
     CACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGAT

6121 CGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAAC
     GCACGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTG

6181 CCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGG
     GGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCC

6241 TTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG
     AAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGAC

6301 GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGG
     CGATTTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCC

6361 GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA
     CATATTCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACT

6421 GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAA
     CTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTT

6481 CATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCC
     GTACACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGG

6541 TGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG
     ACGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATACACCTCTATTC
```

FIG. 62I

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6601 GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG
     CGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAGTTTACGGGCAC

6661 CCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGC
     GGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACG

6721 GCCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATA
     CGGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTAT

6781 CCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCAT
     GGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTA

6841 GCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATC
     CGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAG

6901 ACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC
     TGGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTG

6961 TTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG
     AACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTC

7021 GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGA
     CGTCCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCT

7081 CTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAAT
     GAGGAAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTA

7141 CCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAA
     GGACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATT

7201 CCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTG
     GGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGAC

7261 TCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGT
     AGGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCA

7321 CCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAG
     GGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTC

7381 CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTC
     GAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAG

7441 TGGCTGCCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGA
     ACCGACGGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGGACCTCCCCCT

7501 GCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGC
     CGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCG

7561 GGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTG
     CCTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCAC

7621 CGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCA
     GCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGT

7681 CAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATT
     GTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAA

7741 TGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGC
     ACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCG

7801 GGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCC
     CCGCAGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGG

7861 ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA
     TGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTT
```

FIG. 62J

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7921 GGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAAT
     CCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTA

7981 AGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCG
     TCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGC

8041 TAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGC
     ATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCG

8101 TTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCA
     AAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGT

8161 ATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCC
     TATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGG

8221 AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG
     TTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGC

8281 TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAA
     ATGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTT

8341 GTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTG
     CAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGAC

8401 CGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCAC
     GCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTG

8461 TTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCT
     AACGATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGA

8521 CGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGC
     GCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCG

8581 GAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCC
     CTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGG

8641 ACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCA
     TGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGT

8701 CGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAG
     GCTGCCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTC

8761 AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT
     TCGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTA

8821 GTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTAT
     CAAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATA

8881 AGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCAT
     TCGGTCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTA

8941 AGAACCACTTGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACT
     TCTTGGTGAACTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGA

9001 CCACAGTTACTCTCCAGGTGAAATTAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGT
     GGTGTCAATGAGAGGTCCACTTTAATTATCCCACCGGCGTACGGAGTCTTTTGAACCCCA

9061 ACCGCCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAG
     TGGCGGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTC

9121 AGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCT
     TCCTCCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGA

9181 CAAAC
     GTTTG
```

FIG. 63

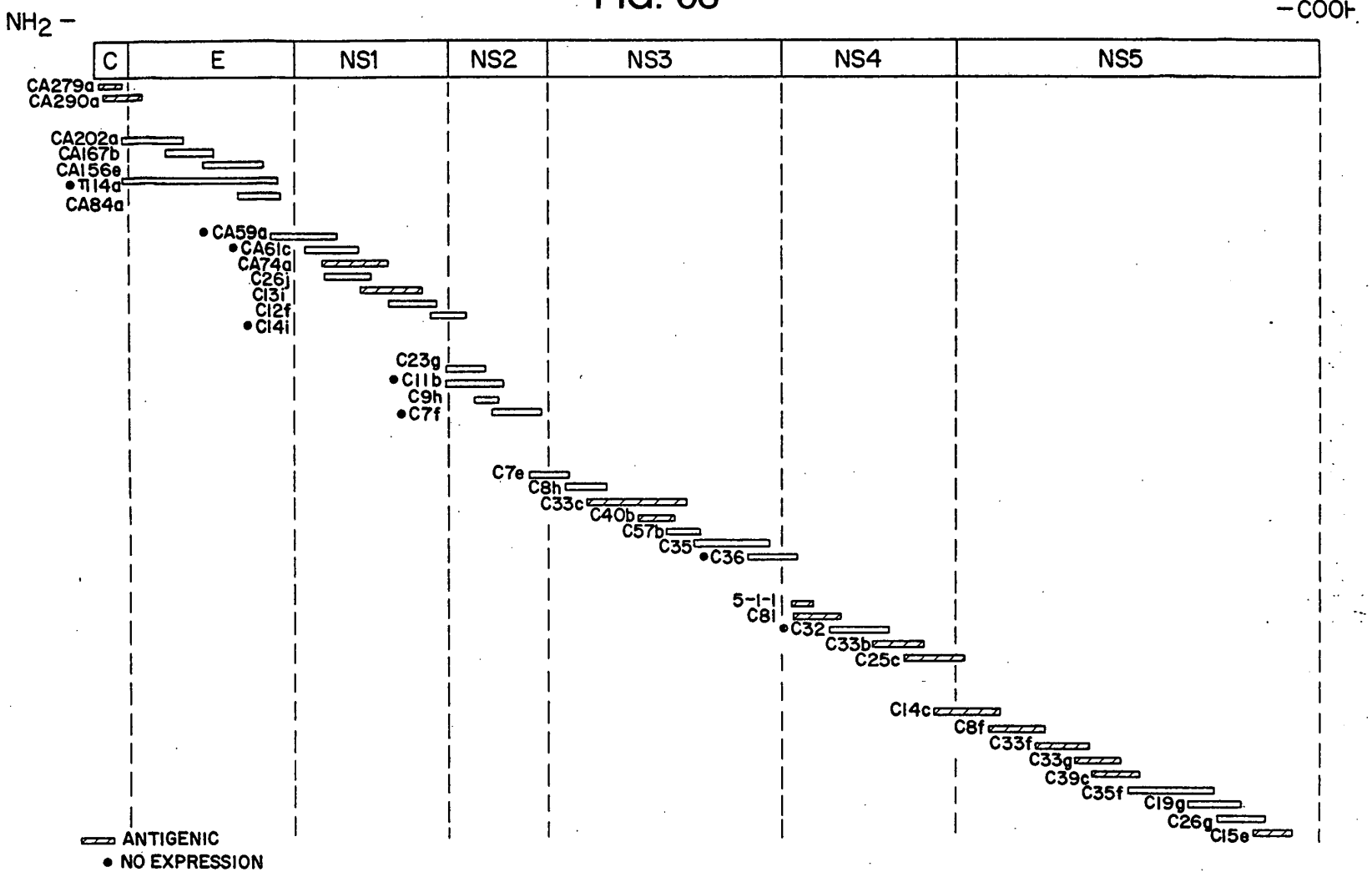
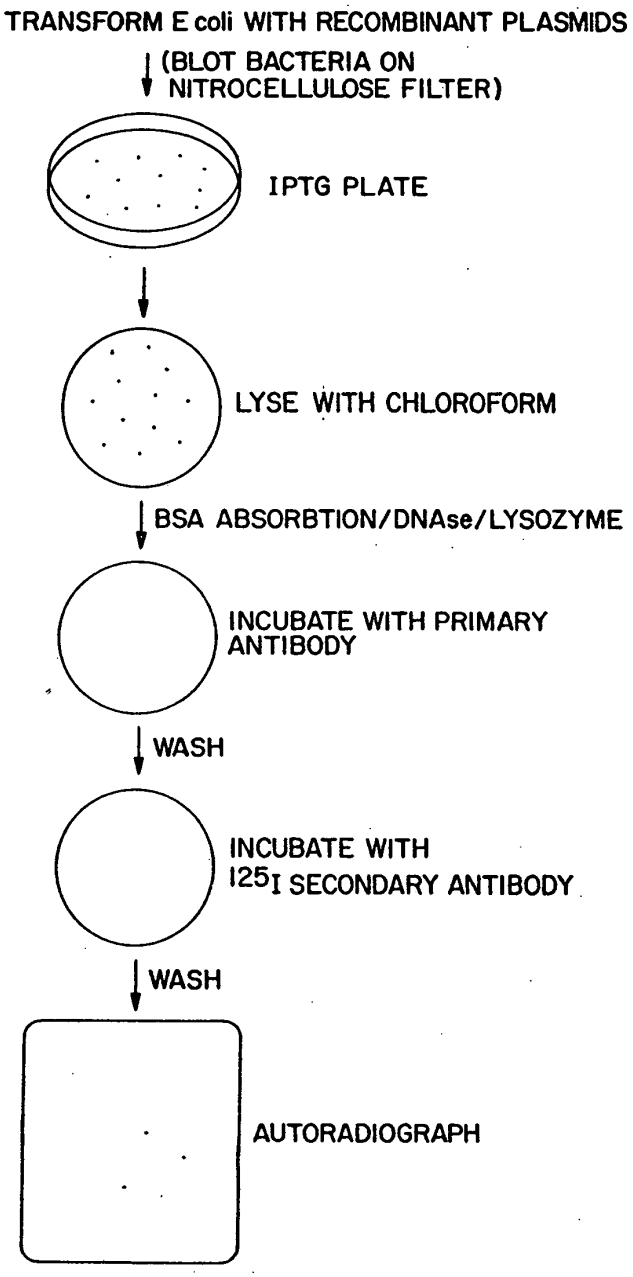
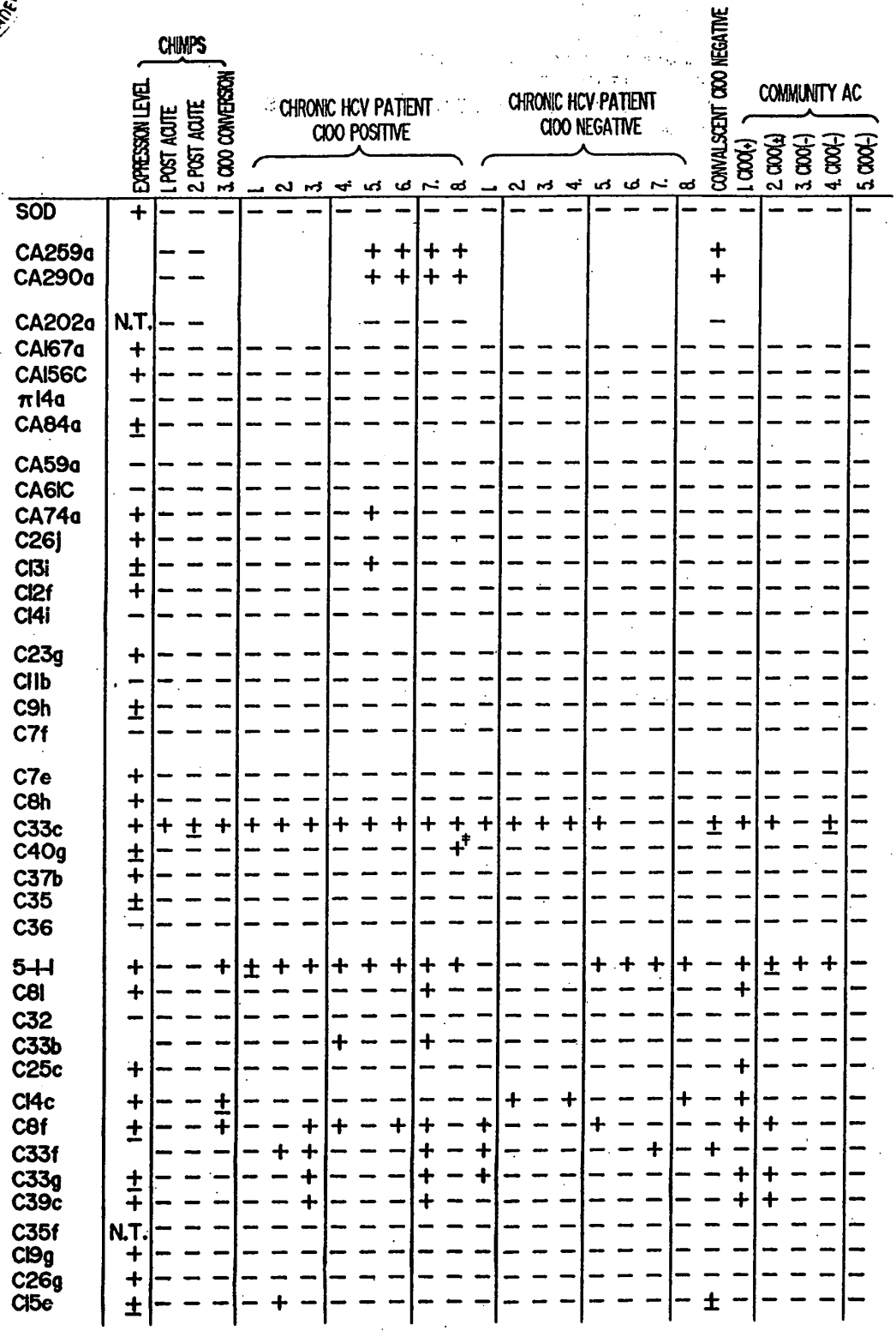


FIG. 64





N.T. = EXPRESSION NOT TESTED
‡ THIS POLYPEPTIDE WAS NEGATIVE IN THIS COLONY SCREEN BUT POSITIVE BY WESTERN BLOT ANALYSIS

FIG. 65

FIG. 66A

```
        R T
MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR
KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP-100
RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA

                          T
LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL-200
YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD
GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT-300

                                        V
TQGCNCSIYPGHITGHRMAWDMMMNWSPTTALVMAQLLRIPQAILDMIAG
AHWGVLAGIAYFSMVGNWAKVLVVLLLFAGVDAETHVTGGSAGHTVSGFV-400
SLLAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWLAGLFYHHKFNSS
GCPERLASCRPLTDFDQGWGPISYANGSGPDQRPYCWHYPPKPCGIVPAK-500
SVCGPVYCFTPSPVVVGTTDRSGAPTYSWGENDTDVFVLNNTRPPLGNWF
GCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPDATYSRCGSG-600

  I
PWLTPRCLVDYPYRLWHYPCTINYTIFKIRMYVGGVEHRLEAACNWTRGE
RCDLEDRDRSELSPLLLTTTQWQVLPCSFTTLPALSTGLIHLHQNIVDVQ-700
YLYGVGSSIASWAIKWEYVVLLFLLLADARVCSCLWMMLLISQAEAALEN
LVILNAASLAGTHGLVSFLVFFCFAWYLKGKWVPGAVYTFYGMWPLLLLL-800

                                                (N)
LALPQRAYALDTEVAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFL
TRVEAQLHVWIPPLNVRGGRDAVILLMCAVHPTLVFDITKLLLAVFGPLN-900
ILQASLLKVPYFVRVQGLLRFCALARKMIGGHYVQMVIIKLGALTGTYVY
NHLTPLRDWAHNGLRDLAVAVEFVVFSQMETKLITWGADTAACGDIINGL-1000
PVSARRGREILLGPADGMVSKGWRLLAPITAYAQQTRGLLGCIITSLTGR
DKNQVEGEVQIVSTAAQTTFATCINGVCWTVYHGAGTRTIASPKGPVIQM-1100
YTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRG
SLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEN-1200
LETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGSGKSTKVPAAYAAQGYK

                          L
VLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFL-1300

ADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATAT
PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKC-1400
DELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS

  Y               (S)
VIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYR-1500
FVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPV
CQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLPYLVAYQATVCARAQAP-1600
PPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEITLTHPVTKYIMTCMS
ADLEVVTSTWVLVGGVLAALAAYCLSTGCVVIVGRVVLSGKPAIIPDREV-1700
LYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAV
QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSP-1800
LTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLID
```

FIG. 66B

```
                                  (G)
ILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAA-1900

                                                        (HC)
ILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSS
LTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTWLKAKLM-2000

                        (V)
PQLPGIPFVSCQRGYKGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPR
TCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEEYVEIRQVGDFH-2100
YVTGMTTDNLKCPCQVPSPEFFTELDGVRLHRFAPPCKPLLREEVSFRVG
LHEYPVGSQLPCEPEPDVAVLTSMLTDPSHITAEAAGRRLARGSPPSVAS-2200
SSASQLSAPSLKATCTANHDSPDAELIEANLLWRQEMGGNITRVESENKV
VILDSFDPLVAEEDEREISVPAEILRKSRRFAQALPVWARPDYNPPLVET-2300

                                                      S
WKKPDYEPPVVHGCPLPPPKSPPVPPPRKKRTVVLTESTLSTALAELATR

                                        (FA)
SFGSSSTSGITGDNTTTSSEPAPSGCPPDSDAESYSSMPPLEGEPGDPDL-2400
SDGSWSTVSSEANAEDVVCCSMSYSWTGALVTPCAAEEQKLPINALSNSL
LRHHNLVYSTTSRSACQRQKKVTFDRLQVLDSHYQDVLKEVKAAASKVKA-2500

(F)
NLLSVEEACSLTPPHSAKSKFGYGAKDVRCHARKAVTHINSVWKDLLEDN
VTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT-2600
KLPLAVMGSSYGFQYSPGQRVEFLVQAWKSKKTPMGFSYDTRCFDSTVTE

                                                (G)
SDIRTEEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCGYRRCR-2700
ASGVLTTSCGNTLTCYIKARAACRAAGLQDCTMLVCGDDLVVICESAGVQ
EDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDGAGKR-2800
VYYLTRDPTTPLARAAWETARHTFVNSWLGNIIMFAPTLWARMILMTHFF
SVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRLHGLSAFSLHSYSPG-2900

                        G
EINRVAACLRKLGVPPLRAWRHRARSVRARLLARGGRAAICGKYLFNWAV
RTKLK----------------(Stop codon not yet reached)
```

( ) = Heterogeneity due to possible 5' or 3' terminal cloning artefacts.

FIG. 67A

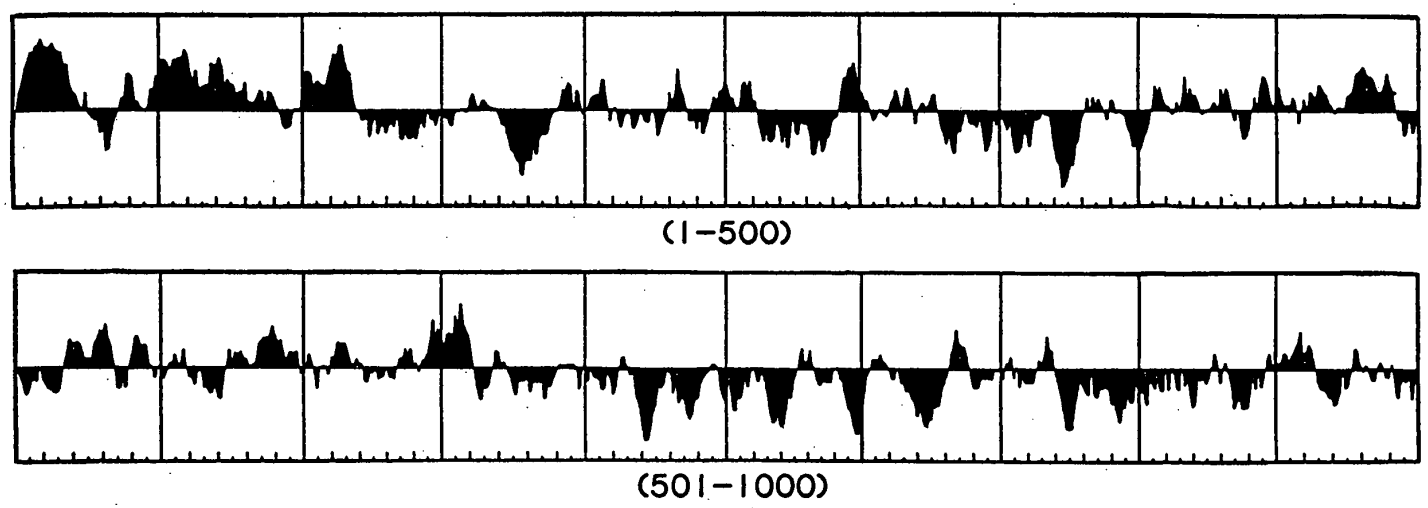


FIG. 67B

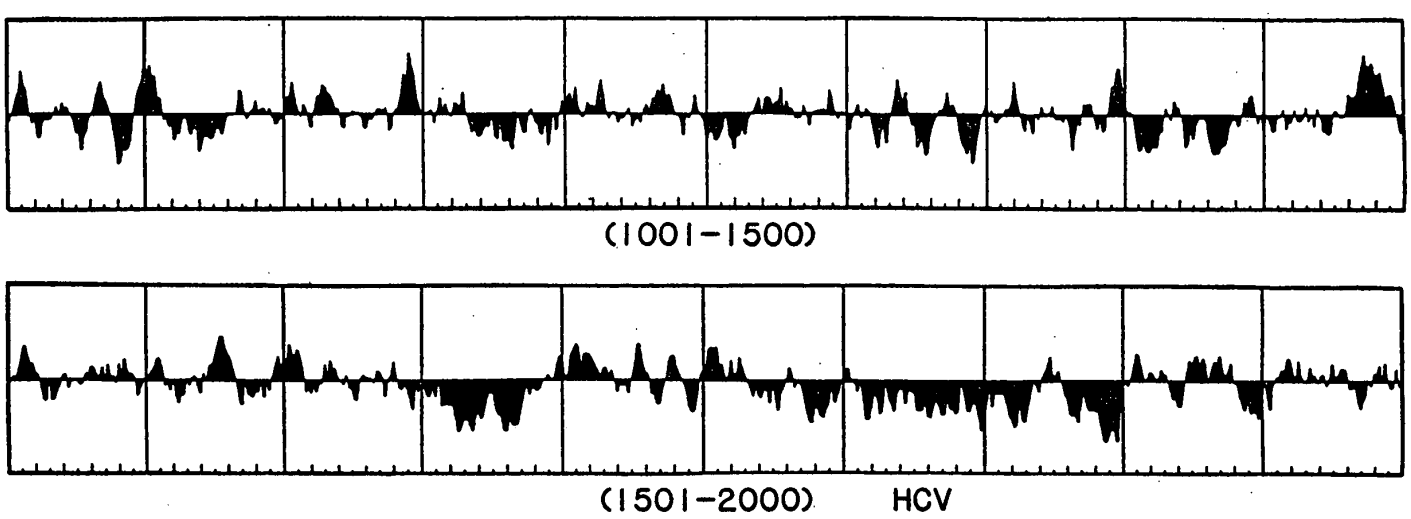


FIG. 67C

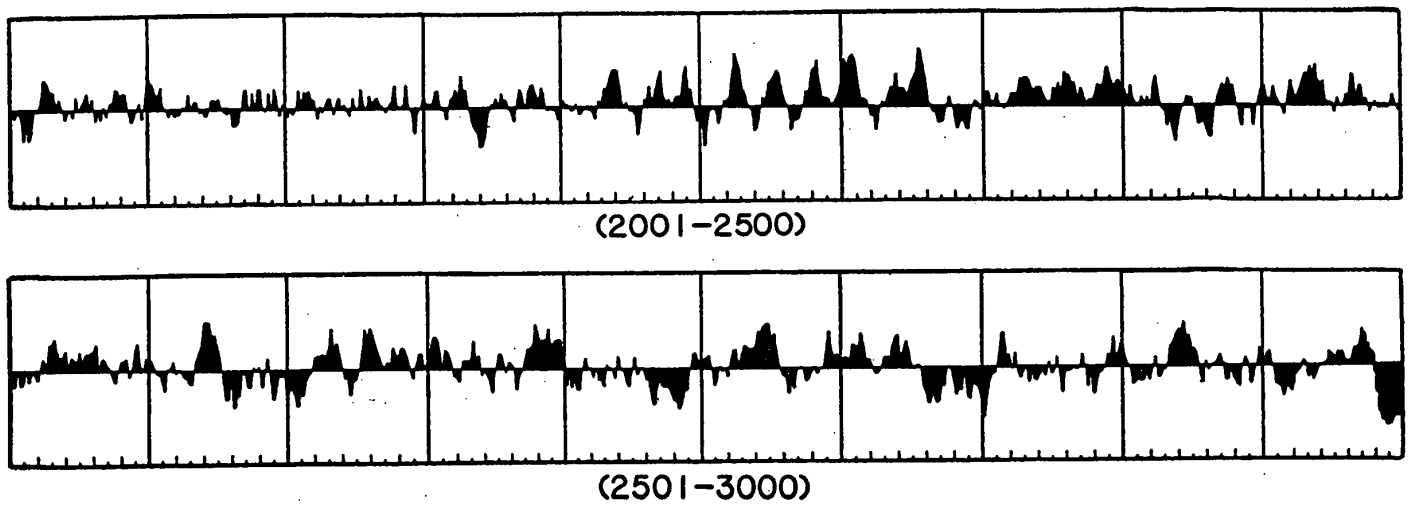
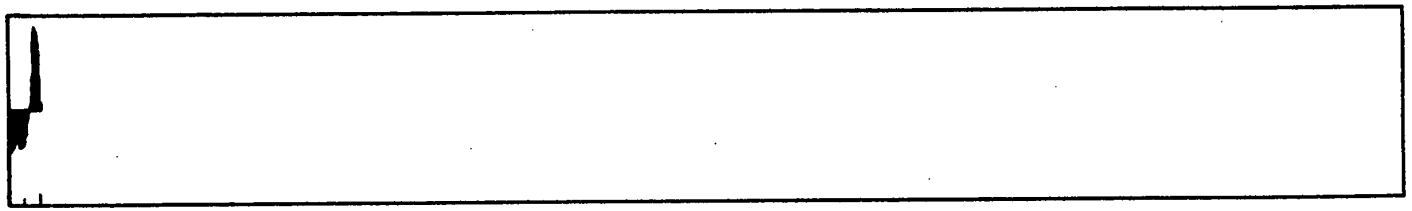


FIG. 67D



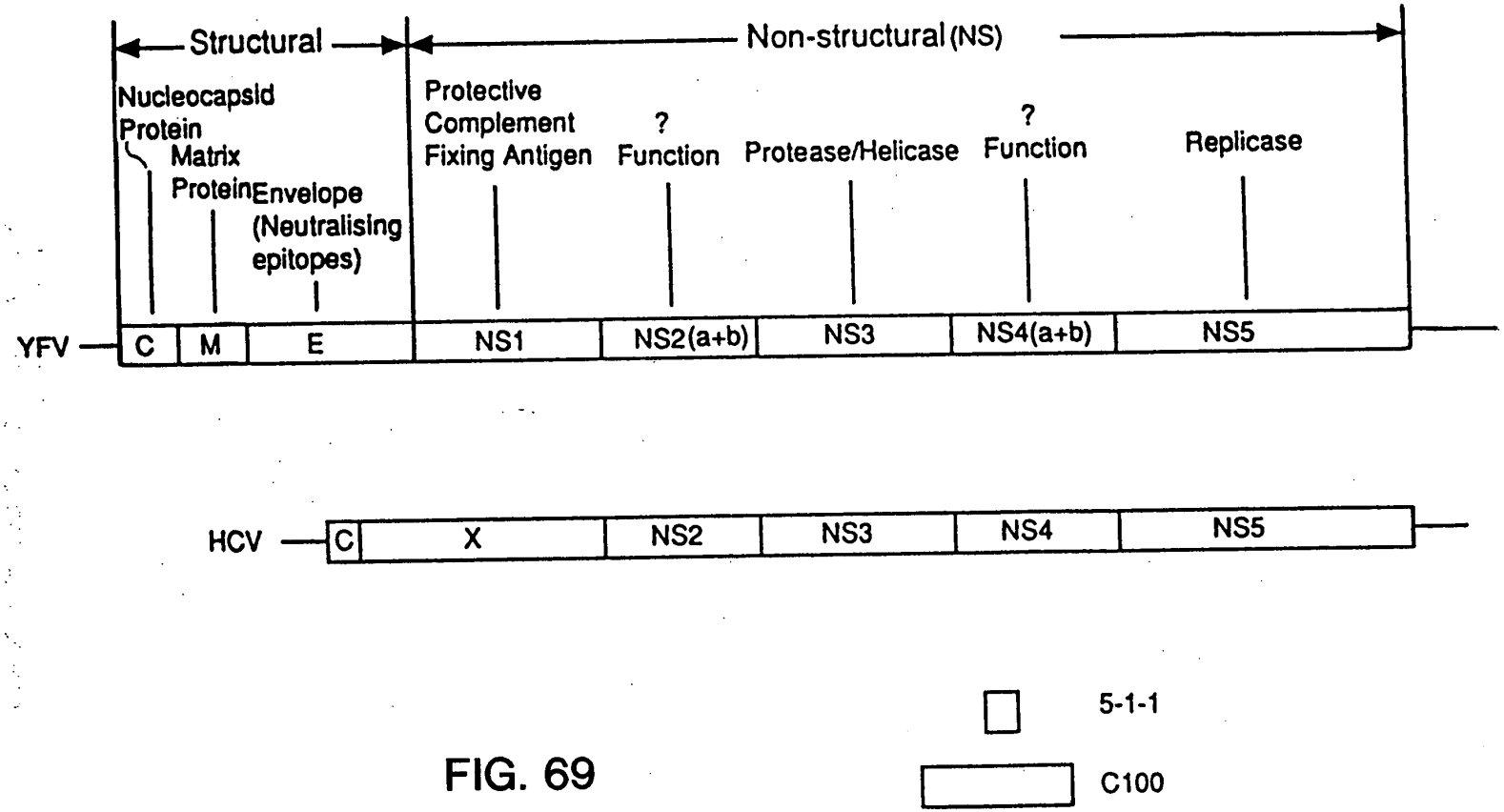


FIG. 69

FIG. 68

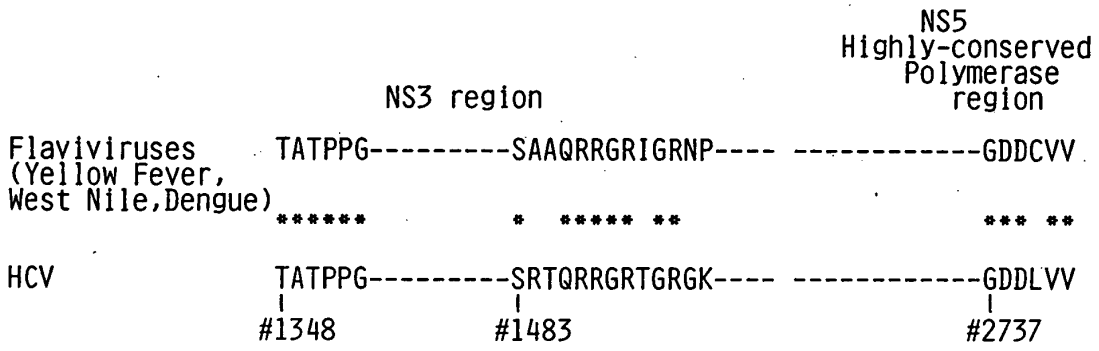


FIG. 73

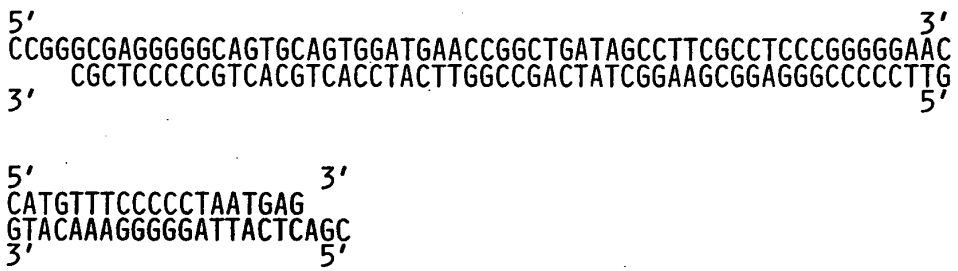


FIG. 70

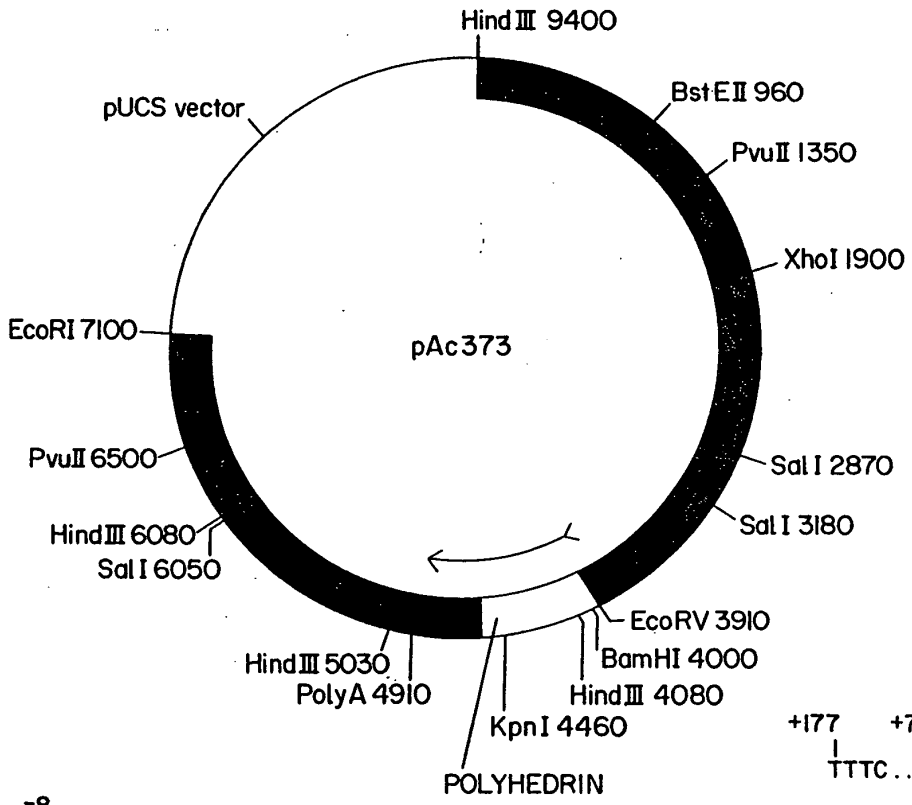


FIG. 71

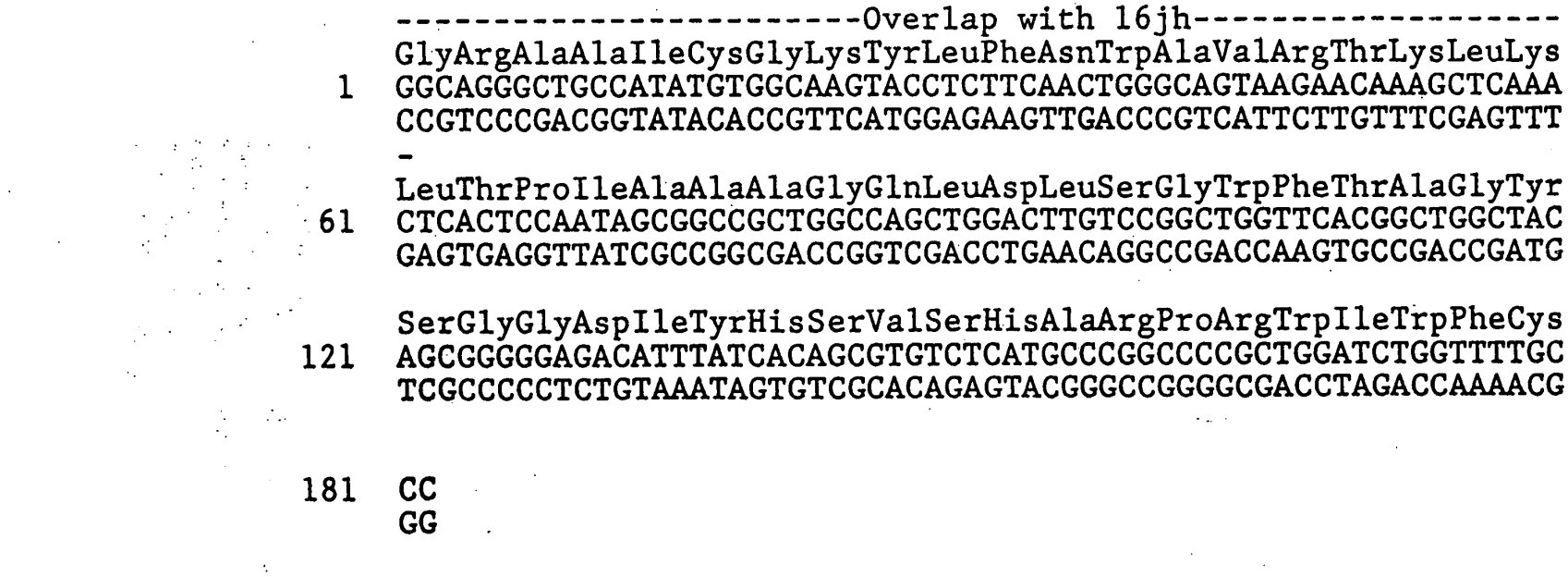


FIG. 72A

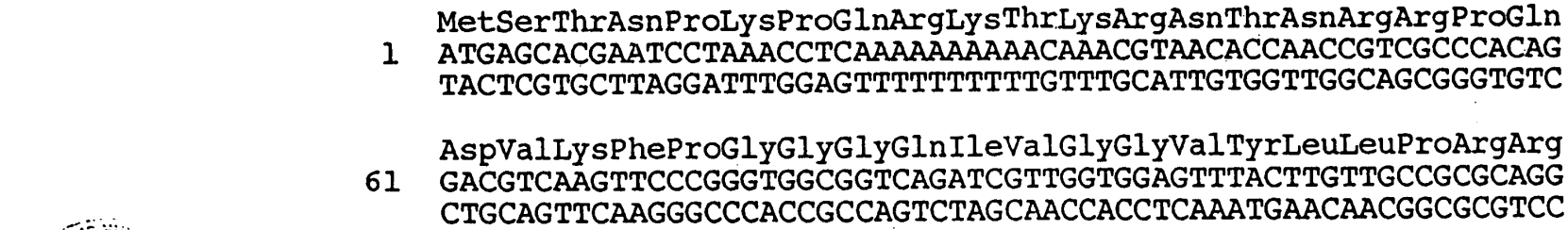


FIG. 72B

```
    GlyProArgLeuGlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGly
121 GGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGT
    CCGGGATCTAACCCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCA

    ArgArgGlnProIleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGly
181 AGACGTCAGCCTATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGG
    TCTGCAGTCGGATAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCC

    TyrProTrpProLeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerPro
241 TACCCTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCC
    ATGGGAACCGGGGAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGG

    ArgGlySerArgProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGly
301 CGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGT
    GCACCGAGAGCCGGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCA

    LysValIleAspThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuVal
361 AAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTC
    TTCCAGTAGCTATGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAG

    GlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAsp
421 GGCGCCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGAC
    CCGCGGGGAGAACCTCCGCGACGGTCCCGGGACCGCGTACCGCAGGCCCAAGACCTTCTG
```

FIG. 72C

```
    GlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIlePheLeuLeuAla
481 GGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCC
    CCGCACTTGATACGTTGTCCCTTGGAAGGACCAACGAGAAAGAGATAGAAGGAAGACCGG

    LeuLeuSerCysLeuThrValProAlaSerAlaTyrGlnValArgAsnSerThrGlyLeu
541 CTGCTCTCTTGCTTGACTGTGCCCGCTTCGGCCTACCAAGTGCGCAACTCCACGGGGCTT
    GACGAGAGAACGAACTGACACGGGCGAAGCCGGATGGTTCACGCGTTGAGGTGCCCCGAA

    TyrHisValThrAsnAspCysProAsnSerSerIleValTyrGluAlaAlaAspAlaIle
601 TACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTACGAGGCGGCCGATGCCATC
    ATGGTGCAGTGGTTACTAACGGGATTGAGCTCATAACACATGCTCCGCCGGCTACGGTAG

    LeuHisThrProGlyCysValProCysValArgGluGlyAsnAlaSerArgCysTrpVal
661 CTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCAACGCCTCGAGGTGTTGGGTG
    GACGTGTGAGGCCCCACGCAGGGAACGCAAGCACTCCCGTTGCGGAGCTCCACAACCCAC

    AlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThrGlnLeuArgArg
721 GCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCCCGCGACGCAGCTTCGACGT
    CGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGGGCGCTGCGTCGAAGCTGCA

    HisIleAspLeuLeuValGlySerAlaThrLeuCysSerAlaLeuTyrValGlyAspLeu
781 CACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTTCGGCCCTCTACGTGGGGGACCTG
    GTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAGCCGGGAGATGCACCCCCTGGAC

    CysGlySerValPheLeuValGlyGlnLeuPheThrPheSerProArgArgHisTrpThr
841 TGCGGGTCTGTCTTTCTTGTCGGCCAACTGTTCACCTTCTCTCCCAGGCGCCACTGGACG
    ACGCCCAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAGAGGGTCCGCGGTGACCTGC
```

FIG. 72D

```
      ThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThrGlyHisArgMetAlaTrp
901   ACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACGGGTCACCGCATGGCATGG
      TGCGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTGCCCAGTGGCGTACCGTACC

      AspMetMetMetAsnTrpSerProThrThrAlaLeuValMetAlaGlnLeuLeuArgIle
961   GATATGATGATGAACTGGTCCCCTACGACGGCGTTGGTAATGGCTCAGCTGCTCCGGATC
      CTATACTACTACTTGACCAGGGGATGCTGCCGCAACCATTACCGAGTCGACGAGGCCTAG

      ProGlnAlaIleLeuAspMetIleAlaGlyAlaHisTrpGlyValLeuAlaGlyIleAla
1021  CCACAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGGAGTCCTGGCGGGCATAGCG
      GGTGTTCGGTAGAACCTGTACTAGCGACCACGAGTGACCCCTCAGGACCGCCCGTATCGC

      TyrPheSerMetValGlyAsnTrpAlaLysValLeuValValLeuLeuLeuPheAlaGly
1081  TATTTCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGTGCTGCTGCTATTTGCCGGC
      ATAAAGAGGTACCACCCCTTGACCCGCTTCCAGGACCATCACGACGACGATAAACGGCCG

      ValAspAlaGluThrHisValThrGlyGlySerAlaGlyHisThrValSerGlyPheVal
1141  GTCGACGCGGAAACCCACGTCACCGGGGGAAGTGCCGGCCACACTGTGTCTGGATTTGTT
      CAGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCACGGCCGGTGTGACACAGACCTAAACAA

      SerLeuLeuAlaProGlyAlaLysGlnAsnValGlnLeuIleAsnThrAsnGlySerTrp
1201  AGCCTCCTCGCACCAGGCGCCAAGCAGAACGTCCAGCTGATCAACACCAACGGCAGTTGG
      TCGGAGGAGCGTGGTCCGCGGTTCGTCTTGCAGGTCGACTAGTTGTGGTTGCCGTCAACC
```

FIG. 72E

```
        HisLeuAsnSerThrAlaLeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeuAlaGly
1261    CACCTCAATAGCACGGCCCTGAACTGCAATGATAGCCTCAACACCGGCTGGTTGGCAGGG
        GTGGAGTTATCGTGCCGGGACTTGACGTTACTATCGGAGTTGTGGCCGACCAACCGTCCC

        LeuPheTyrHisHisLysPheAsnSerSerGlyCysProGluArgLeuAlaSerCysArg
1321    CTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGA
        GAAAAGATAGTGGTGTTCAAGTTGAGAAGTCCGACAGGACTCTCCGATCGGTCGACGGCT

        ProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGlyPro
1381    CCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCC
        GGGGAATGGCTAAAACTGGTCCCGACCCCGGGATAGTCAATACGGTTGCCTTCGCCGGGG

        AspGlnArgProTyrCysTrpHisTyrProProLysProCysGlyIleValProAlaLys
1441    GACCAGCGCCCCTACTGCTGGCACTACCCCCCAAAACCTTGCGGTATTGTGCCCGCGAAG
        CTGGTCGCGGGGATGACGACCGTGATGGGGGGTTTTGGAACGCCATAACACGGGCGCTTC

        SerValCysGlyProValTyrCysPheThrProSerProValValValGlyThrThrAsp
1501    AGTGTGTGTGGTCCGGTATATTGCTTCACTCCCAGCCCCGTGGTGGTGGGAACGACCGAC
        TCACACACACCAGGCCATATAACGAAGTGAGGGTCGGGGCACCACCACCCTTGCTGGCTG

        ArgSerGlyAlaProThrTyrSerTrpGlyGluAsnAspThrAspValPheValLeuAsn
1561    AGGTCGGGCGCGCCCACCTACAGCTGGGGTGAAAATGATACGGACGTCTTCGTCCTTAAC
        TCCAGCCCGCGCGGGTGGATGTCGACCCCACTTTTACTATGCCTGCAGAAGCAGGAATTG
```

FIG.72F

```
      AsnThrArgProProLeuGlyAsnTrpPheGlyCysThrTrpMetAsnSerThrGlyPhe
1621  AATACCAGGCCACCGCTGGGCAATTGGTTCGGTTGTACCTGGATGAACTCAACTGGATTC
      TTATGGTCCGGTGGCGACCCGTTAACCAAGCCAACATGGACCTACTTGAGTTGACCTAAG

      ThrLysValCysGlyAlaProProCysValIleGlyGlyAlaGlyAsnAsnThrLeuHis
1681  ACCAAAGTGTGCGGAGCGCCTCCTTGTGTCATCGGAGGGGCGGGCAACAACACCCTGCAC
      TGGTTTCACACGCCTCGCGGAGGAACACAGTAGCCTCCCCGCCCGTTGTTGTGGGACGTG

      CysProThrAspCysPheArgLysHisProAspAlaThrTyrSerArgCysGlySerGly
1741  TGCCCCACTGATTGCTTCCGCAAGCATCCGGACGCCACATACTCTCGGTGCGGCTCCGGT
      ACGGGGTGACTAACGAAGGCGTTCGTAGGCCTGCGGTGTATGAGAGCCACGCCGAGGCCA


      ProTrpLeuThrProArgCysLeuValAspTyrProTyrArgLeuTrpHisTyrProCys
1801  CCCTGGATCACACCCAGGTGCCTGGTCGACTACCCGTATAGGCTTTGGCATTATCCTTGT
      GGGACCTAGTGTGGGTCCACGGACCAGCTGATGGGCATATCCGAAACCGTAATAGGAACA

      ThrIleAsnTyrThrIlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeu
1861  ACCATCAACTACACCATATTTAAAATCAGGATGTACGTGGGAGGGGTCGAACACAGGCTG
      TGGTAGTTGATGTGGTATAAATTTTAGTCCTACATGCACCCTCCCCAGCTTGTGTCCGAC

      GluAlaAlaCysAsnTrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSer
1921  GAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCTGGAAGACAGGGACAGGTCC
      CTTCGACGGACGTTGACCTGCGCCCCGCTTGCAACGCTAGACCTTCTGTCCCTGTCCAGG

      GluLeuSerProLeuLeuLeuThrThrThrGlnTrpGlnValLeuProCysSerPheThr
1981  GAGCTCAGCCCGTTACTGCTGACCACTACACAGTGGCAGGTCCTCCCGTGTTCCTTCACA
      CTCGAGTCGGGCAATGACGACTGGTGATGTGTCACCGTCCAGGAGGGCACAAGGAAGTGT
```

FIG. 72G

```
     ThrLeuProAlaLeuSerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGln
2041 ACCCTACCAGCCTTGTCCACCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAG
     TGGGATGGTCGGAACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAACACCTGCACGTC

     TyrLeuTyrGlyValGlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValVal
2101 TACTTGTACGGGGTGGGGTCAAGCATCGCGTCCTGGGCCATTAAGTGGGAGTACGTCGTT
     ATGAACATGCCCCACCCCAGTTCGTAGCGCAGGACCCGGTAATTCACCCTCATGCAGCAA

     LeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeu
2161 CTCCTGTTCCTTCTGCTTGCAGACGCGCGCGTCTGCTCCTGCTTGTGGATGATGCTACTC
     GAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGACGAACACCTACTACGATGAG

     IleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAla
2221 ATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCC
     TATAGGGTTCGCCTCCGCCGAAACCTCTTGGAGCATTATGAATTACGTCGTAGGGACCGG

     GlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrpTyrLeuLysGly
2281 GGGACGCACGGTCTTGTATCCTTCCTCGTGTTCTTCTGCTTTGCATGGTATTTGAAGGGT
     CCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAAACGTACCATAAACTTCCCA

     LysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeuLeuLeuLeuLeu
2341 AAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTGGCCTCTCCTCCTGCTCCTG
     TTCACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACCGGAGAGGAGGACGAGGAC
```

FIG. 72H

```
     LeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAlaSerCysGlyGly
2401 TTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGTGGCCGCGTCGTGTGGCGGT
     AACCGCAACGGGGTCGCCCGCATGCGCGACCTGTGCCTCCACCGGCGCAGCACACCGCCA

     ValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyrIleSer
2461 GTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCACCATATTACAAGCGCTATATCAGC
     CAACAAGAGCAGCCCAACTACCGCGACTGAGACAGTGGTATAATGTTCGCGATATAGTCG

     TrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHisValTrp
2521 TGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGGAAGCGCAACTGCACGTGTGG
     ACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTGCACACC

     IleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeuMetCysAlaVal
2581 ATTCCCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCATCTTACTCATGTGTGCTGTA
     TAAGGGGGGGAGTTGCAGGCTCCCCCCGCGCTGCGGCAGTAGAATGAGTACACACGACAT

     HisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPheGlyProLeuTrp
2641 CACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCCGTCTTCGGACCCCTTTGG
     GTGGGCTGAGACCATAAACTGTAGTGGTTTAACGACGACCGGCAGAAGCCTGGGGAAACC

     IleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGlnGlyLeuLeuArg
2701 ATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGCGTCCAAGGCCTTCTCCGG
     TAAGAAGTTCGGTCAAACGAATTTCATGGGATGAAACACGCGCAGGTTCCGGAAGAGGCC
```

FIG. 721

```
          PheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMetValIleIleLys
2761      TTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATCATTAAG
          AAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAGTAATTC

          LeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAla
2821      TTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGACTGGGCG
          AATCCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTGAGGAGAAGCCCTGACCCGC

          HisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPheSerGlnMetGlu
2881      CACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTTCTCCCAAATGGAG
          GTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAGCAGAAGAGGGTTTACCTC

          ThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeu
2941      ACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGGTGACATCATCAACGGCTTG
          TGGTTCGAGTAGTGCACCCCCCGTCTATGGCGGCGCACGCCACTGTAGTAGTTGCCGAAC

          ProValSerAlaArgArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSer
3001      CCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCCAGCCGATGGAATGGTCTCC
          GGACAAAGGCGGGCGTCCCCGGCCCTCTATGACGAGCCCGGTCGGCTACCTTACCAGAGG

          LysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeu
3061      AAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCAGCAGACAAGGGGCCTCCTA
          TTCCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGTCGTCTGTTCCCCGGAGGAT

          GlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGln
3121      GGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCCAG
          CCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTTGGTTCACCTCCCACTCCAGGTC
```

FIG. 72J

```
      IleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThr
3181  ATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCATCAATGGGGTGTGCTGGACT
      TAACACAGTTGACGACGGGTTTGGAAGGACCGTTGCACGTAGTTACCCCACACGACCTGA

      ValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyProValIleGlnMet
3241  GTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAAGGGTCCTGTCATCCAGATG
      CAGATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGGTTCCCAGGACAGTAGGTCTAC

      TyrThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeu
3301  TATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAGGTAGCCGCTCATTG
      ATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGCGTTCCATCGGCGAGTAAC

      ThrProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIle
3361  ACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATT
      TGTGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCAGTGCTCCGTGCGGCTACAGTAA

      ProValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyr
3421  CCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTCGCCCCGGCCCATTTCCTAC
      GGGCACGCGGCCGCCCCACTATCGTCCCCGTCGGACGACAGCGGGGCCGGGTAAAGGATG

      LeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePhe
3481  TTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGGGCACGCCGTGGGCATATTT
      AACTTTCCGAGGAGCCCCCCAGGCGACAACACGGGGCGCCCCGTGCGGCACCCGTATAAA

      ArgAlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIleProValGluAsn
3541  AGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGACTTTATCCCTGTGGAGAAC
      TCCCGGCGCCACACGTGGGCACCTCACCGATTCCGCCACCTGAAATAGGGACACCTCTTG
```

FIG. 72K

```
     LeuGluThrThrMetArgSerProValPheThrAspAsnSerSerProProValValPro
3601 CTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTCCTCTCCACCAGTAGTGCCC
     GATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAGGAGAGGTGGTCATCACGGG

     GlnSerPheGlnValAlaHisLeuHisAlaProThrGlySerGlyLysSerThrLysVal
3661 CAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAGCGGCAAAAGCACCAAGGTC
     GTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTCGCCGTTTTCGTGGTTCCAG

     ProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsnProSerValAlaAla
3721 CCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAACCCCTCTGTTGCTGCA
     GGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTGGGGAGACAACGACGT

     ThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThr
3781 ACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACC
     TGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCCTGG

     GlyValArgThrIleThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeu
3841 GGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCTT
     CCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAA

     AlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSer
3901 GCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGTGACGAGTGCCACTCC
     CGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACACTGCTCACGGTGAGG
```

FIG. 72L

```
      ThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGly
3961  ACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGACCAAGCAGAGACTGCGGGG
      TGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACTGGTTCGTCTCTGACGCCCC

      AlaArgLeuValValLeuAlaThrAlaThrProProGlySerValThrValProHisPro
4021  GCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTCACTGTGCCCCATCCC
      CGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAGTGACACGGGGTAGGG

      AsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIle
4081  AACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTTTACGGCAAGGCTATC
      TTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAAATGCCGTTCCGATAG

      ProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCys
4141  CCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCATTCAAAGAAGAAGTGC
      GGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTAAGTTTCTTCTTCACG

      AspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGly
4201  GACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGT
      CTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCA

      LeuAspValSerValIleProThrSerGlyAspValValValValAlaThrAspAlaLeu
4261  CTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTGGCAACCGATGCCCTC
      GAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGGAG
```

FIG. 72M

```
      MetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThrCysValThrGln
4321  ATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTGTCACCCAG
      TACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTC

      ThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThrLeuProGlnAsp
4381  ACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATCACGCTCCCCCAGGAT
      TGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAGTGCGAGGGGGTCCTA

      AlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArg
4441  GCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGA
      CGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTCGGTCCGTAGATGTCT

      PheValAlaProGlyGluArgProSerGlyMetPheAspSerSerValLeuCysGluCys
4501  TTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCCGTCCTCTGTGAGTGC
      AAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACG

      TyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArg
4561  TATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACTACAGTTAGGCTACGA
      ATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGATGTCAATCCGATGCT

      AlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGly
4621  GCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGC
      CGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAACTTAAAACCCTCCCG

      ValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGly
4681  GTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGG
      CAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCC
```

FIG. 72N

```
      GluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaPro
4741  GAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCT
      CTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGA

      ProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGly
4801  CCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAGCCCACCCTCCATGGG
      GGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCC

      ProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisPro
4861  CCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATCACCCTGACGCACCCA
      GGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGT

      ValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluValValThrSerThrTrp
4921  GTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTCGTCACGAGCACCTGG
      CAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACC

      ValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysVal
4981  GTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTGTCAACAGGCTGCGTG
      CACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGACAGTTGTCCGACGCAC

      ValIleValGlyArgValValLeuSerGlyLysProAlaIleIleProAspArgGluVal
5041  GTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTC
      CAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAG

      LeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGln
5101  CTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAA
      GAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTT
```

FIG. 72O

```
      GlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSer
5161  GGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCC
      CCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGG

      ArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPhe
5221  CGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAAAAACTCGAGACCTTC
      GCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAG

      TrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThr
5281  TGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTGGCGGGCTTGTCAACG
      ACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAACCGCCCGAACAGTTGC

      LeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerPro
5341  CTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCTGCTGTCACCAGCCCA
      GACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGACGACAGTGGTCGGGT

      LeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeu
5401  CTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCCAGCTC
      GATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACCCACCGACGGGTCGAG

      AlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGly
5461  GCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGC
      CGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGACCGCGGCGGTAGCCG
```

FIG. 72P

```
          SerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAla
5521      AGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTATGGCGCGGGCGTGGCG
          TCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCCGCACCGC

          GlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerThrGluAspLeuVal
5581      GGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGGACCTGGTC
          CCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGGTGCCTCCTGGACCAG

          AsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyValValCysAlaAla
5641      AATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCA
          TTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCGCACCAGACACGTCGT

          IleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIle
5701      ATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGGATGAACCGGCTGATA
          TATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACCTACTTGGCCGACTAT

          AlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrValProGluSerAspAla
5761      GCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTGCCGGAGAGCGATGCA
          CGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCACGGCCTCTCGCTACGT

          AlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeu
5821      GCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTG
          CGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTCGAGGACTCCGCTGAC
```

FIG. 72Q

```
          HisGlnTrpIleSerSerGluCysThrThrProCysSerGlySerTrpLeuArgAspIle
5881      CACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCCTGGCTAAGGGACATC
          GTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAG

          TrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMet
5941      TGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATG
          ACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGATTTTCGATTCGAGTAC

          ProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArg
6001      CCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGA
          GGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATATTCCCCCAGACCGCT


          ValAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLys
6061      GTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAA
          CACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTT

          AsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPhe
6121      AACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTC
          TTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTACACCTCACCCTGGAAG

          ProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPhe
6181      CCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCGCCGAACTACACGTTC
          GGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGCGGCTTGATGTGCAAG
```

FIG. 72R

```
      AlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHis
6241  GCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAGGCAGGTGGGGGACTTCCAC
      CGCGATACCTCCCACAGACGTCTCCTTATACACCTCTATTCCGTCCACCCCCTGAAGGTG

      TyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnValProSerProGlu
6301  TACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTGCCAGGTCCCATCGCCCGAA
      ATGCACTGCCCATACTGATGACTGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTT

      PhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProProCysLysProLeu
6361  TTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCCCCCTGCAAGCCCTTG
      AAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGGGGGACGTTCGGGAAC

      LeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProValGlySerGlnLeu
6421  CTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCGGTAGGGTCGCAATTA
      GACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGCCATCCCAGCGTTAAT

      ProCysGluProGluProAspValAlaValLeuThrSerMetLeuThrAspProSerHis
6481  CCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTCACTGATCCCTCCCAT
      GGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAGTGACTAGGGAGGGTA

      IleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProProSerValAlaSer
6541  ATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCCCCCTCTGTGGCCAGC
      TATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGGGGGAGACACCGGTCG
```

FIG. 72S

```
      SerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThrAlaAsnHisAsp
6601  TCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGCACCGCTAACCATGAC
      AGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACGTGGCGATTGGTACTG

      SerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGlyAsn
6661  TCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGGCGGCAAC
      AGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTCCTCTACCCGCCGTTG

      IleThrArgValGluSerGluAsnLysValValIleLeuAspSerPheAspProLeuVal
6721  ATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCCTTCGATCCGCTTGTG
      TAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGGAAGCTAGGCGAACAC

      AlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArgLysSerArgArg
6781  GCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTGCGGAAGTCTCGGAGA
      CGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGACGCCTTCAGAGCCTCT

      PheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProProLeuValGluThr
6841  TTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCCCCGCTAGTGGAGACG
      AAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGGGGCGATCACCTCTGC

      TrpLysLysProAspTyrGluProProValValHisGlyCysProLeuProProProLys
6901  TGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGTCCGCTTCCACCTCCAAAG
      ACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACAGGCGAAGGTGGAGGTTTC

      SerProProValProProProArgLysLysArgThrValValLeuThrGluSerThrLeu
6961  TCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTCACTGAATCAACCCTA
      AGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAGTGACTTAGTTGGGAT
```

FIG. 72T

```
      SerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerSerThrSerGlyIle
7021  TCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCCTCAACTTCCGGCATT
      AGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAA

      ThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyCysProProAspSer
7081  ACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGCTGCCCCCCCGACTCC
      TGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCGACGGGGGGGCTGAGG


      AspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProGlyAspProAspLeu
7141  GACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCTGGGGATCCGGATCTT
      CTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGACCCCTAGGCCTAGAA

      SerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGluAspValValCysCys
7201  AGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAGGATGTCGTGTGCTGC
      TCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTCCTACAGCACACGACG

      SerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAlaAlaGluGluGlnLys
7261  TCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCCGCGGAAGAACAGAAA
      AGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGGCGCCTTCTTGTCTTT

      LeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsnLeuValTyrSerThr
7321  CTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAATTTGGTGTATTCCACC
      GACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTAAACCACATAAGGTGG
```

FIG. 72U

```
      ThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAspArgLeuGlnValLeu
7381  ACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGACAGACTGCAAGTTCTG
      TGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTGTCTGACGTTCAAGAC

      AspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAlaSerLysValLysAla
7441  GACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCGTCAAAAGTGAAGGCT
      CTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGCAGTTTTCACTTCCGA

      AsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHisSerAlaLysSerLys
7501  AACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACACTCAGCCAAATCCAAG
      TTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTGAGTCGGTTTAGGTTC

      PheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAlaValThrHisIleAsn
7561  TTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCCGTAACCCACATCAAC
      AAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGGCATTGGGTGTAGTTG

      SerValTrpLysAspLeuLeuGluAspAsnValThrProIleAspThrThrIleMetAla
7621  TCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGACACTACCATCATGGCT
      AGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTGTGATGGTAGTACCGA

      LysAsnGluValPheCysValGlnProGluLysGlyGlyArgLysProAlaArgLeuIle
7681  AAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAGCCAGCTCGTCTCATC
      TTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTCGGTCGAGCAGAGTAG

      ValPheProAspLeuGlyValArgValCysGluLysMetAlaLeuTyrAspValValThr
7741  GTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTGTACGACGTGGTTACA
      CACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAACATGCTGCACCAATGT
```

FIG. 72V

```
      LysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGlnArg
7801  AAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATACTCACCAGGACAGCGG
      TTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATGAGTGGTCCTGTCGCC

      ValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAsp
7861  GTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGAT
      CAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTACCCCAAGAGCATACTA

      ThrArgCysPheAspSerThrValThrGluSerAspIleArgThrGluGluAlaIleTyr
7921  ACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTAC
      TGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCTCCGTTAGATG

      GlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeu
7981  CAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCCCTCACCGAGAGGCTT
      GTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGGGAGTGGCTCTCCGAA


      TyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArg
8041  TATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCCGC
      ATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCGATAGCGTCCACGGCG

      AlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArg
8101  GCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGG
      CGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACGATGTAGTTCCGGGCC
```

FIG. 72W

```
      AlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeu
8161  GCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCGACGACTTA
      CGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCACACACCGCTGCTGAAT

      ValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSerLeuArgAlaPheThr
8221  GTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGCCTGAGAGCCTTCACG
      CAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCGGACTCTCGGAAGTGC

      GluAlaMetThrArgTyrSerAlaProProGlyAspProProGlnProGluTyrAspLeu
8281  GAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAACCAGAATACGACTTG
      CTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTTGGTCTTATGCTGAAC

      GluLeuIleThrSerCysSerSerAsnValSerValAlaHisAspGlyAlaGlyLysArg
8341  GAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGACGGCGCTGGAAAGAGG
      CTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTGCCGCGACCTTTCTCC

      ValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAlaAlaTrpGluThrAla
8401  GTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCTGCGTGGGAGACAGCA
      CAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGACGCACCCTCTGTCGT

      ArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPheAlaProThrLeuTrp
8461  AGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTTGCCCCCACACTGTGG
      TCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAACGGGGGTGTGACACC
```

FIG. 72X

```
      AlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAlaArgAspGlnLeuGlu
8521  GCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCCAGGGACCAGCTTGAA
      CGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGGTCCCTGGTCGAACTT

      GlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGluProLeuAspLeuPro
8581  CAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAACCACTTGATCTACCT
      GTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTTGGTGAACTAGATGGA

      ProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHisSerTyrSerProGly
8641  CCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCACAGTTACTCTCCAGGT
      GGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTGTCAATGAGAGGTCCA

      GluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValProProLeuArgAlaTrp
8701  GAAATTAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCGCCCTTGCGAGCTTGG
      CTTTAATTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGCGGGAACGCTCGAACC

      ArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGlyGlyArgAlaAlaIle
8761  AGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGAGGCAGGGCTGCCATA
      TCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCTCCGTCCCGACGGTAT

      CysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLysLeuThrProIleAla
8821  TGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAACTCACTCCAATAGCG
      ACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTTGAGTGAGGTTATCGC
```

FIG. 72Y

```
      AlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyrSerGlyGlyAspIle
8881  GCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTACAGCGGGGGAGACATT
      CGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATGTCGCCCCCTCTGTAA

      TyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
8941  TATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGCCC
      ATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACGGG
```

```
    GluPheGlySerValIleProThrSerGlyAspValValValValAlaThrAspAlaLeu
 1  GAATTCGGGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTGGCAACCGATGCCCTC
    CTTAAGCCCAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGGAG

    1 ECOR1, 7 NLA1V, 8 AVA2 SAU96, 15 FOK1, 24 NSPB11, 26 FNU4H
    1, 52 SFAN1, 57 MNL1, 60 NLA111,

    MetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThrCysValThrGln
61  ATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTGTCACCCAG
    TACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTC

    65 HPA11, 74 HPA11, 83 TAQ1, 85 HINF1, 90 HPH, 106 AFL111 MA
    E2, 112 MAE3, 113 HPH,

    ThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThrLeuProGlnAsp
121 ACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATCACGCTCCCCCAAGAT
    TGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAGTGCGAGGGGGTTCTA

    125 TAQ1, 149 HPH, 178 SFAN1,

    AlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArg
181 GCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGA
    CGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTCGGTCCGTAGATGTCT

    198 MAE2, 226 ECOR11 SCRF1, 230 SFAN1,

    PheValAlaProGlyGluArgProProAlaCysSerThrArgProSerSerValSerAla
241 TTTGTGGCACCGGGGGAGCGCCCTCCGGCATGTTCGACTCGTCCGTCCTCTGTGAGTGCC
    AAACACCGTGGCCCCCTCGCGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGG

    246 BAN1 NLA1V, 250 HPA11 NCI1 SCRF1, 257 HAE11, 258 HHA1, 2
    62 MNL1, 265 HPA11, 268 NSPC1, 269 NLA111, 274 TAQ1, 276 HIN
    F1, 287 MNL1, 296 BSP1286,

    ArgIle
301 CGAATTC
    GCTTAAG

    302 ECOR1,

361
```

FIG. 74

FIG. 75

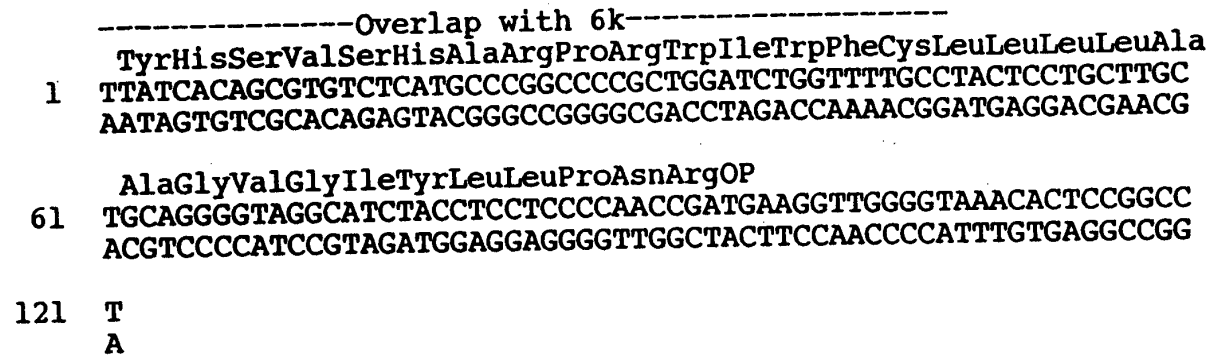


FIG. 76

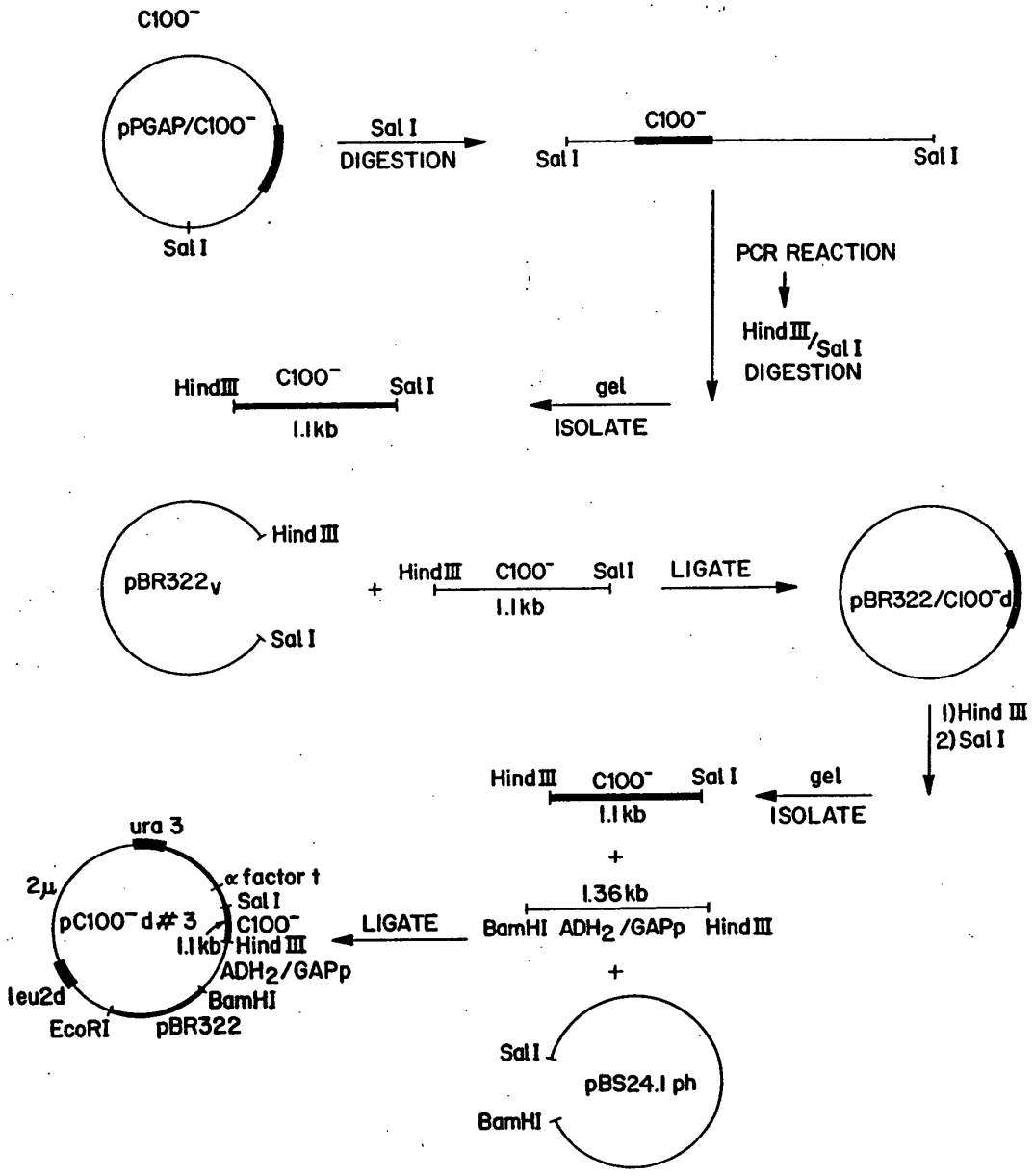


FIG. 77

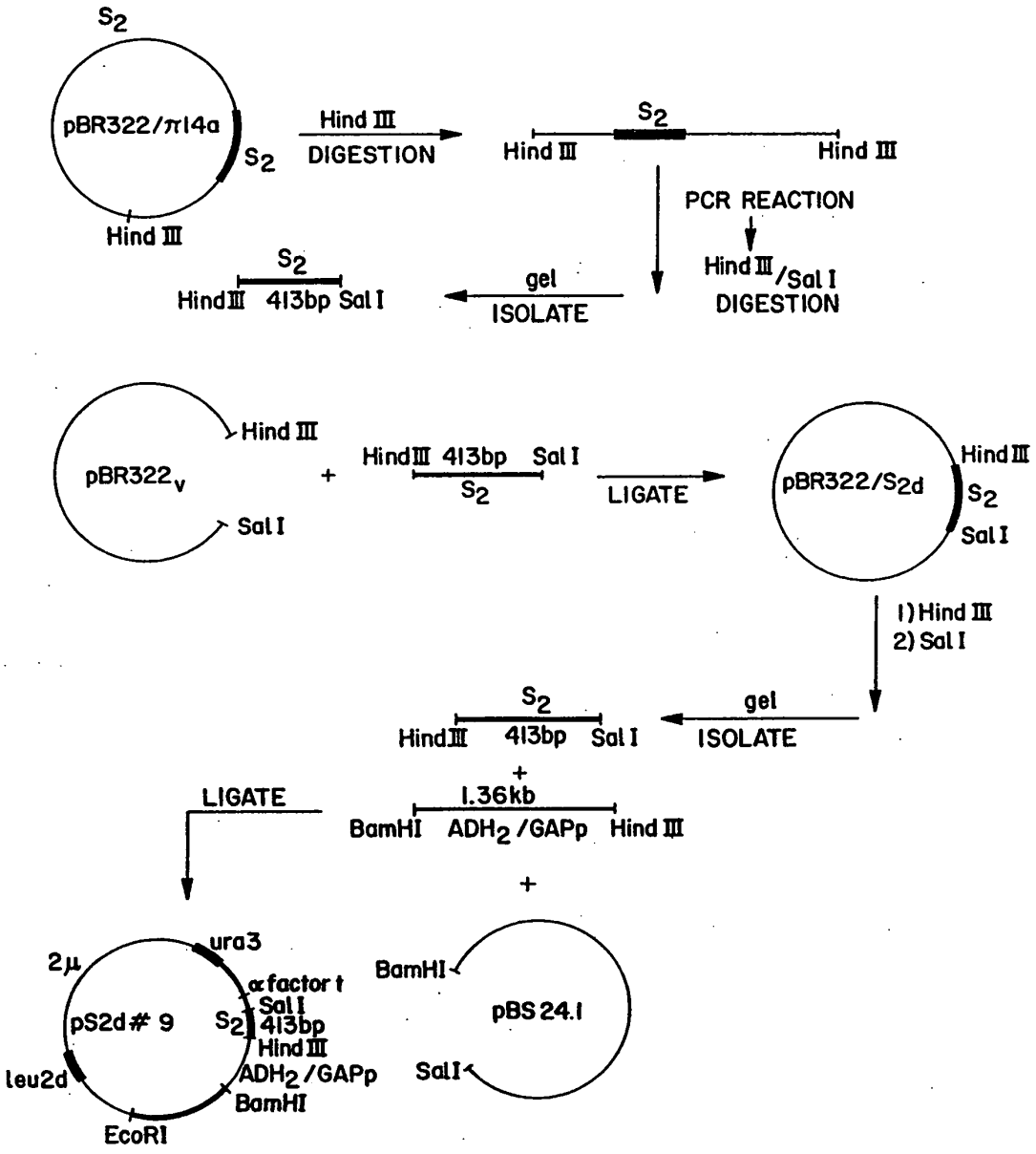


FIG. 78

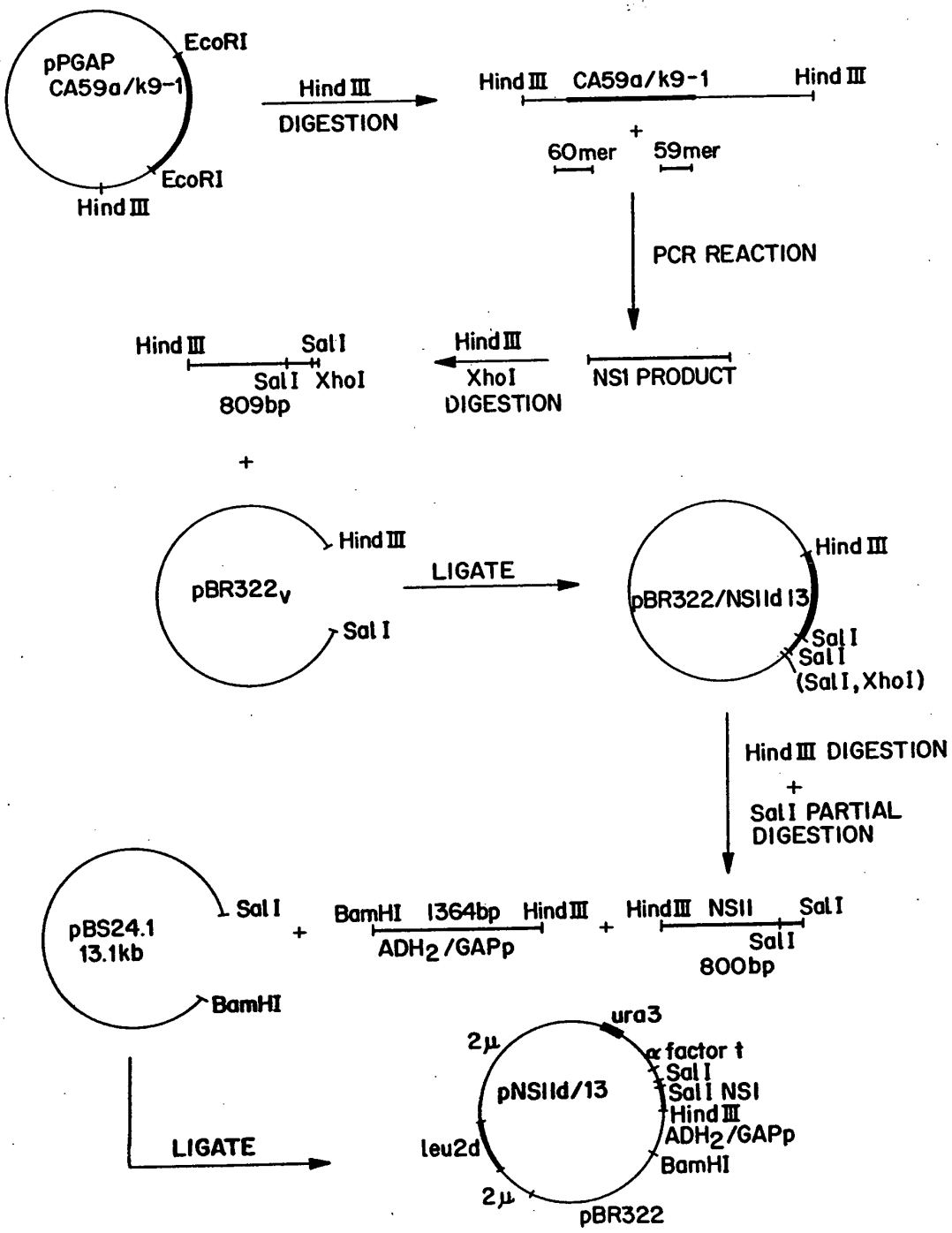


FIG. 79A

AlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThr
2 GCGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACG
CGCCACCTGAAATAGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACAAGTGC

29 MAE1, 40 NLA111, 43 MNL1, 45 AVA2 NLA1V SAU96, 49 NCI1 SC
RF1, 50 HPA11,

AspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaPro
62 GATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCC
CTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGG

69 MNL1, 83 BSP1286, 92 ALU1, 97 ECOR11 SCRF1, 106 HPH, 109
MNL1, 113 NLA111,

ThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysVal
122 ACAGGCAGCGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTG
TGTCCGTCGCCGTTTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATATTCCAC

126 BBV FNU4H1, 127 NSPB11, 129 FNU4H1, 145 AVA2 NLA1V SAU96
, 148 NCI1 SCRF1, 149 HPA11, 152 BBV FNU4H1, 156 NDE1, 161 B
BV FNU4H1, 163 ALU1, 165 DDE1,

LeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAla
182 CTAGTACTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCT
GATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGA

182 MAE1, 184 SCA1, 185 RSA1, 195 MNL1, 203 BBV FNU4H1, 228
AFL111 NSPC1, 229 NLA111,

HisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIle
242 CATGGGATCGATCCTAACATCAGGACCGGGGGTGAGAACAATTACCACTGGCAGCCCCATC
GTACCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAG

242 NLA111, 246 BIN1, 247 MBO1 SAU3A, 248 CLA1, 249 TAQ1, 25
1 BIN1 MBO1 SAU3A, 264 AVA2 SAU96, 267 HPA11 NCI1 SCRF1, 271
HPH, 291 BBV FNU4H1,

ThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAsp
302 ACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGAC
TGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTG

302 MAE2, 304 RSA1, 340 BSP1286 HGIA, 343 AVA1, 350 HAE11, 3
51 HHA1,

IleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThr
362 ATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACT
TATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGA

372 MAE3, 391 FOK1, 392 SFAN1, 399 FOK1,

ValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrPro
422 GTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCT
CAGGAACTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGA

431 TTHIII2, 435 ALWN1, 461 BSP1286 HGIA, 479 MNL1,

FIG. 79B

ProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGly
482 CCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGA
GGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCT

482 HPA11 NCI1 SCRF1, 484 BAN11 BSP1286, 485 NLA1V, 491 MAE3
, 497 BSP1286, 503 FOK1, 513 TAQ1, 515 MNL1, 518 MNL1, 537 H
PA11,

GluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeu
542 GAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTC
CTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAG

543 XHO2, 544 BIN1 MBO1 SAU3A, 571 MNL1, 573 TAQ1,

IlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGly
602 ATCTTCTGTCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGC
TAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCG

603 MBO11, 619 MBO11, 638 FNU4H1, 645 ALU1, 660 SFAN1,

IleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAsp
662 ATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGAT
TAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTA

672 HAE1, 673 HAE111, 682 NSPB11 SAC2, 683 THA1, 693 AFL111
MAE2, 703 FOK1, 712 NSPB11, 714 FNU4H1,

ValValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVal
722 GTTGTCGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTG
CAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCAC

740 SFAN1, 745 MNL1, 748 NLA111, 753 HPA11, 762 HPA11, 771 T
AQ1, 773 HINF1, 778 HPH,

IleAspCysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThr
782 ATAGACTGCAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACC
TATCTGACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGG

794 AFL111 MAE2, 800 MAE3, 801 HPH, 813 TAQ1, 837 HPH,

IleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThr
842 ATTGAGACAATCACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACT
TAACTCTGTTAGTGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGA

866 SFAN1, 886 MAE2,

GlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMet
902 GGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATG
CCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTAC

914 ECOR11 SCRF1, 918 SFAN1, 934 BAN1 NLA1V, 938 HPA11 NCI1
SCRF1, 945 HAE11, 946 HHA1, 948 BGL1, 951 MNL1, 954 HPA11, 9
57 NSPC1, 958 NLA111,

PheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThr
962 TTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACG
AAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGC

963 TAQ1, 965 HINF1, 976 MNL1, 992 HGA1, 1003 TTHIII2, 1013
BAN11 BSP1286 HGIA SAC1, 1014 ALU1,

FIG. 79C

1051 RSA1, 1054 NLA111, 1063 AVA1 NCI1 SCRF1 SMA1, 1064 HPA1
1 NCI1 SCRF1, 1081 ECOR11 SCRF1,

GlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHis
1082 CAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCAC
GTCCTGGTAGAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTG

1084 AVA2 SAU96, 1103 MNL1, 1106 AHA11, 1107 HGA1, 1117 HAE1
STU1, 1118 HAE111, 1120 MNL1, 1133 SFAN1,

PheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAla
1142 TTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCC
AAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGG

1183 ECOR11 SCRF1, 1192 RSA1, 1201 DRA3,

ThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeu
1202 ACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTG-
TGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAAC

1209 HHA1, 1212 MAE1, 1215 BAN11 BSP1286, 1226 MNL1, 1239 NL
A1V, 1240 AVA2 SAU96, 1256 TTHIII2, 1261 HINF1,

IleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaVal
1262 ATTCGCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTT
TAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAA

1267 MNL1, 1279 MNL1, 1282 NCO1, 1283 NLA111, 1286 SAU96, 12
87 HAE111, 1313 HAE11, 1314 HHA1,

GlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAla
1322 CAGAATGAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCC
GTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGG

1332 HPH, 1339 HGA1, 1349 MAE3, 1350 HPH, 1363 NLA111, 1367
NSPC1, 1368 NLA111, 1369 AVA3 NSI1, 1371 NSPC1, 1372 NLA111,
1377 CFR1 XMA3, 1378 HAE111,

AspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAla
1382 GACCTGGAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCC
CTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGG

1384 ECOR11 SCRF1, 1385 GSU1, 1388 MNL1, 1394 MAE3, 1399 BSP
1286 HGIA, 1404 ECOR11 SCRF1, 1409 BSP1286 HGIA, 1419 FNU4H1
, 1421 AHA11, 1422 HGA1, 1426 ECOR11 SCRF1, 1430 BBV FNU4H1,
1437 CFR1, 1438 HAE111, 1439 FNU4H1, 1441 THA1,

AlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLys
1442 GCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAG
CGCATAACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTC

1453 HINCI1, 1461 BBV FNU4H1, 1494 HPA11 NCI1 SCRF1, 1501 NA
E1,

ProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCys
1502 CCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGC
GGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACG

1502 HPA11, 1528 MNL1, 1542 TAQ1, 1553 MBO11, 1558 BSP1286 H
GIA,

SerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLys
1562 TCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAG
AGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTC

1563 DDE1. 1576 RSA1, 1581 TAQ1, 1590 FOK1, 1594 SFAN1, 1612

FIG. 79D

TTHIII2, 1621 HAE111 SAU96,

AlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGln
1622 GCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAG
CGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTC

1624 MNL1, 1628 HAE111, 1630 MNL1, 1634 PST1, 1639 TTHIII1, 1642 THA1, 1643 HGA1, 1658 MNL1,

ThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGly
1682 ACCAACTGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGG
TGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCC

1697 AVA1 XHO1, 1698 TAQ1, 1718 NDE1,

IleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMet
1742 ATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATG
TATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTAC-

1762 HINC11, 1768 BBV FNU4H1, 1772 ECOR11 SCRF1, 1775 BSTE2, 1776 MAE3,

AlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIle
1802 GCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATA
CGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTAT

1809 ALWN1 NSPB11 PVU11, 1810 ALU1, 1811 BBV FNU4H1, 1817 MAE3, 1818 HPH, 1836 MAE1, 1846 MNL1, 1849 MNL1, 1851 MBO11,

LeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGly
1862 TTGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGC
AACCCCCCCCACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCG

1877 BBV FNU4H1, 1884 ALU1, 1889 FNU4H1, 1895 NCI1 SCRF1, 1896 HPA11, 1898 BAN1 NLA1V, 1901 FNU4H1, 1919 HAE11, 1920 HHA1,

AlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIle
1922 GCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATC
CGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAG

1927 DDE1, 1930 ALU1, 1934 AHA11 BAN1 HAE11 NAR1 NLA1V, 1935 HHA1, 1937 FNU4H1, 1966 AVA2 SAU96, 1969 MNL1, 1978 FOK1,

LeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGly
1982 CTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGT
GAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCA

1995 HHA1, 1996 THA1, 2010 BAN11 BSP1286 HGIA SAC1, 2011 ALU1, 2021 BSM1, 2029 MBO1 SAU3A, 2032 NLA111, 2039 HPH,

GluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAla
2042 GAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCC
CTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGG

2042 MNL1, 2044 AVA2 NLA1V SAU96, 2049 MNL1, 2057 MNL1, 2059 AVA2 SAU96, 2060 TTHIII1, 2062 ECOR11 SCRF1, 2083 FOK1, 2086 MNL1, 2093 NCI1 SCRF1, 2094 HPA11, 2096 NLA1V, 2097 BAN11 BSP1286, 2101 MNL1,

LeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGly
2102 CTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGG
GAGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCC

2123 BBV FNU4H1, 2134 HHA1, 2136 NAE1, 2137 HPA11, 2142 MAE2, 2147 HAE111 SAU96, 2149 AVA1 NCI1 SCRF1 SMA1, 2150 HPA11 N

FIG. 79E

CI1 SCRF1, 2156 MNL1,

AlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer
2162 GCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCC
CGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGG

2172 FOK1, 2179 HPA11, 2196 MNL1, 2199 AVA1 NCI1 SCRF1 SMA1,
2200 HPA11 NCI1 SCRF1, 2205 NLAIV, 2210 NLA111,

2222

FIG. 80A

Human 23

```
    GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyArgAla
  1 GGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCCGTGCC
    ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn
 61 AGGGCCCTGGCGCACGGCGTCCGGGTTTTGGAAGACGGCGTGAACTATGCAACAGGGAAC
           CG    A
    LeuProGlyCysSerPheSerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValPro
121 CTTCCTGGTTGCTCCTTTTCTATCTTCCTTCTGGCCCTACTCTCTTGCCTGACCGTGCCC
                      GA                    T
    AlaSerAlaTyrGlnValArgAsnSerThrGlyLeuTyrHisValThrAsnAspCysPro
181 GCTTCAGCCTACCAAGTGCGCAACTCTACGGGGCTTTACCATGTCACCAATGATTGCCCT
    AsnSerSerIleValTyrGluAlaAlaAspAlaIleLeuHisAlaProGlyCysValPro
241 AACTCGAGTATTGTGTACGAGGCGGCCGATGCCATCCTGCACGCTCCGGGGTGTGTCCCT
                      T                                C
    CysValArgGluAspAsnValSerArgCysTrpValAlaValThrProThrValAlaThr
301 TGCGTTCGCGAGGATAACGTCTCGAGATGTTGGGTGGCGGTGACCCCCACGGTGGCCACC
          G                                                    T
    LysAspGlyLysLeuProThrThrGlnLeuArgArgHisIleAspLeuLeuValGlySer
361 AAGGACGGCAAACTCCCCACAACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGC
                                                   C        A
    AlaThrLeuCysSerAlaLeuTyrValGlyAspLeuCysGlySerIlePheLeuValGly
421 GCCACCCTCTGCTCGGCCCTCTACGTGGGGGACCTTTGCGGGTCCATCTTTCTTGTCGGT
          T

    GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCysAsnCysSerIle
481 CAACTGTTTACCTTCTCTCCCAGGCGCCACTGGACGACGCAGGACTGCAACTGTTCTATC
                                                   C
```

FIG. 80B

```
     TyrProGlyHisIleThrGlyHisArgMetAlaTrpAspMetMetMetAsnTrpSerPro
541  TATCCCGGCCATATAACGGGTCACCGCATGGCATGGGATATGATGATGAACTGGTCCCCT
                                                              G
     ThrAlaAlaLeuValValAlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIle
601  ACGGCGGCATTGGTAGTAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATC
                   G    AG
     AlaGlyAlaHisTrpGlyValLeuAlaGlyMetAlaTyrPheSerMetValGlyAsnTrp
661  GCTGGTGCTCACTGGGGAGTCCTGGCGGGCATGGCGTATTTCTCCATGGTGGGGAACTGG
                                                    G
     AlaLysValLeuValValLeuLeuLeuPheAlaGlyValAspAlaGluThrHisArgThr
721  GCGAAGGTCCTGGTAGTGCTGCTTCTATTTGCCGGCGTCGACGCGGAAACCCACCGTACC
                                                         G
     GlyGlySerAlaAlaArgSerThrAlaGlyValAlaSerLeuPheThrProGlyAlaArg
781  GGGGGAAGTGCCGCCCGCAGCACGGCTGGAGTTGCTAGTCTCTTCACACCAGGCGCTAGG
     C           T    A
     GlnAsnIleGlnLeuIleAsnThrAsnGlySerTrpHisIleAsnSerThrAlaLeuAsn
841  CAGAACATCCAGCTGATCAACACCAACGGCAGTTGGCACATCAATAGTACGGCCTTGAAC
                                                              AT
     CysAsnAspSerLeuThrThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn
901  TGCAATGACAGCCTTACCACCGGCTGGTTAGCGGGGCTTTTCTATCACCATAAATTCAAC
       A                                   A

     SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAlaGln
961  TCTTCAGGCTGTCCCGAGAGGTTGGCCAGCTGCCGACCCCTCACCGATTTTGCCCAGG
      G  A                                          G
```

FIG. 81A

Human 27

```
    GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAla
1   GGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCTCCTCTTGGGGGCGCTGCC

    ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn
61  AGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGGAAC

    LeuProGlyCysSerPheSerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValPro
121 CTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCTCTGCTCTCTTGCCTGACCGTGCCC

    AlaSerAlaTyrGlnValArgAsnSerSerGlyIleTyrHisValThrAsnAspCysPro
181 GCATCGGCCTACCAAGTACGCAACTCCTCGGGCATTTACCATGTCACCAATGATTGCCCT

    AsnSerSerIleValTyrGluThrAlaAspThrIleLeuHisSerProGlyCysValPro
241 AATTCGAGTATTGTGTACGAGACGGCCGACACCATCCTACACTCTCCGGGGTGTGTCCCT
      C           C                                             -
    CysValArgGluGlyAsnAlaSerLysCysTrpValProValAlaProThrValAlaThr
301 TGCGTTCGCGAGGGTAACGCCTCGAAATGTTGGGTGCCGGTAGCCCCCACAGTGGCCACC
          G
    ArgAspGlyAsnLeuProAlaThrGlnLeuArgArgHisIleAspLeuLeuValGlySer
361 AGGGACGGCAACCTCCCCGCAACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGT
                                        G         G

    AlaThrLeuCysSerAlaLeuTyrValGlyAspLeuCysGlySerValPheLeuValGly
421 GCCACCCTTTGCTCGGCCCTCTATGTGGGGGACTTGTGCGGGTCTGTCTTTCTTGTCGGT
        C                                                   C

    GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCysAsnCysSerIle
481 CAACTGTTCACTTTCTCCCCCAGGCGCCACTGGACAACGCAAGATTGCAACTGCTCTATC
                  A
```

FIG. 81B

```
     TyrProGlyHisIleThrGlyHisArgMetAlaTrpAspMetMetMetAsnTrpSerPro
541  TACCCCGGCCATATAACGGGACACCGCATGGCATGGGATATGATGATGAACTGGTCCCCT

     ThrAlaAlaLeuValMetAlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIle
601  ACAGCAGCGCTGGTAATGGCTCAGCTGCTCAGGATCCCGCAAGCCATCTTGGACATGATC
          G

     AlaGlyAlaHisTrpGlyValLeuAlaGlyIleAlaTyrPheSerMetValGlyAsnTrp
661  GCTGGTGCTCACTGGGGAGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGG

     AlaLysValLeuValValLeuLeuLeuPheAlaGlyValAspAlaThrThrTyrThrThr
721  GCGAAGGTCCTGGTGGTGCTGTTGCTGTTTGCCGGCGTCGATGCGACAACCTATACCACC

     GlyGlyAsnAlaAlaArgThrThrGlnAlaLeuThrSerPhePheSerProGlyAlaLys
781  GGGGGGAATGCTGCCAGGACCACGCAGGCGCTCACCAGTTTTTTCAGCCCAGGCGCCAAG

     GlnAspIleGlnLeuIleAsnThrAsnGlySerTrpHisIleAsnArgThrAlaLeuAsn
841  CAGGATATCCAGCTGATCAACACCAACGGCAGTTGGCACATCAATCGCACGGCCTTGAAC
      G                              T

     CysAsnAlaSerLeuAspThrGlyTrpValAlaGlyLeuPheTyrTyrHisLysPheAsn
901  TGTAATGCGAGCCTCGACACTGGCTGGGTAGCGGGGCTCTTCTATTACCACAAATTCAAC
                  T                    G

     SerSerGlyCysProGluArgMetAlaSerCysArgProLeuAlaAspPheAspGln
961  TCTTCAGGCTGCCCCGAGAGGATGGCCAGCTGTAGGCCCCTTGCCGATTTCGACCAGG
                                                          C
```

FIG. 82A

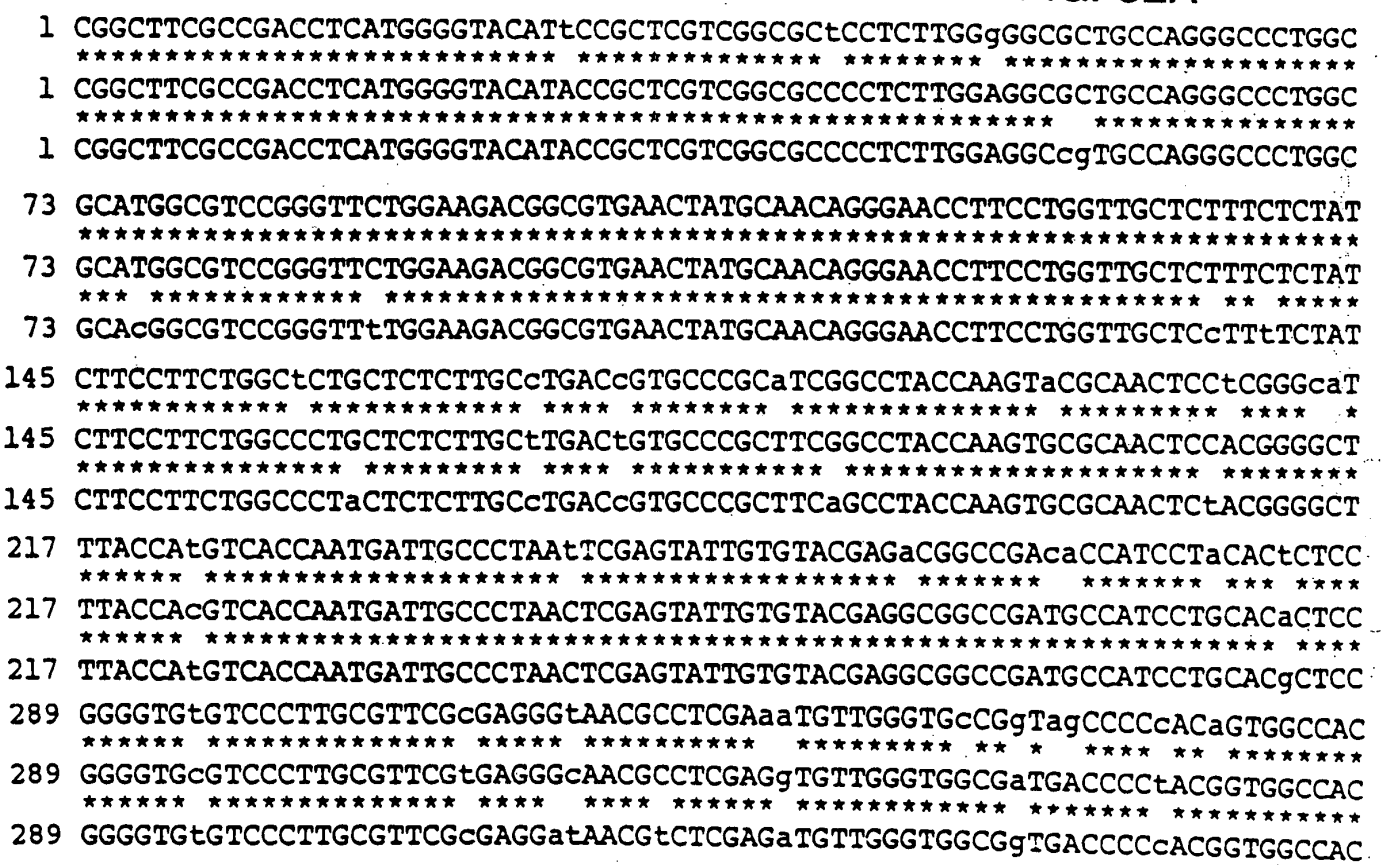
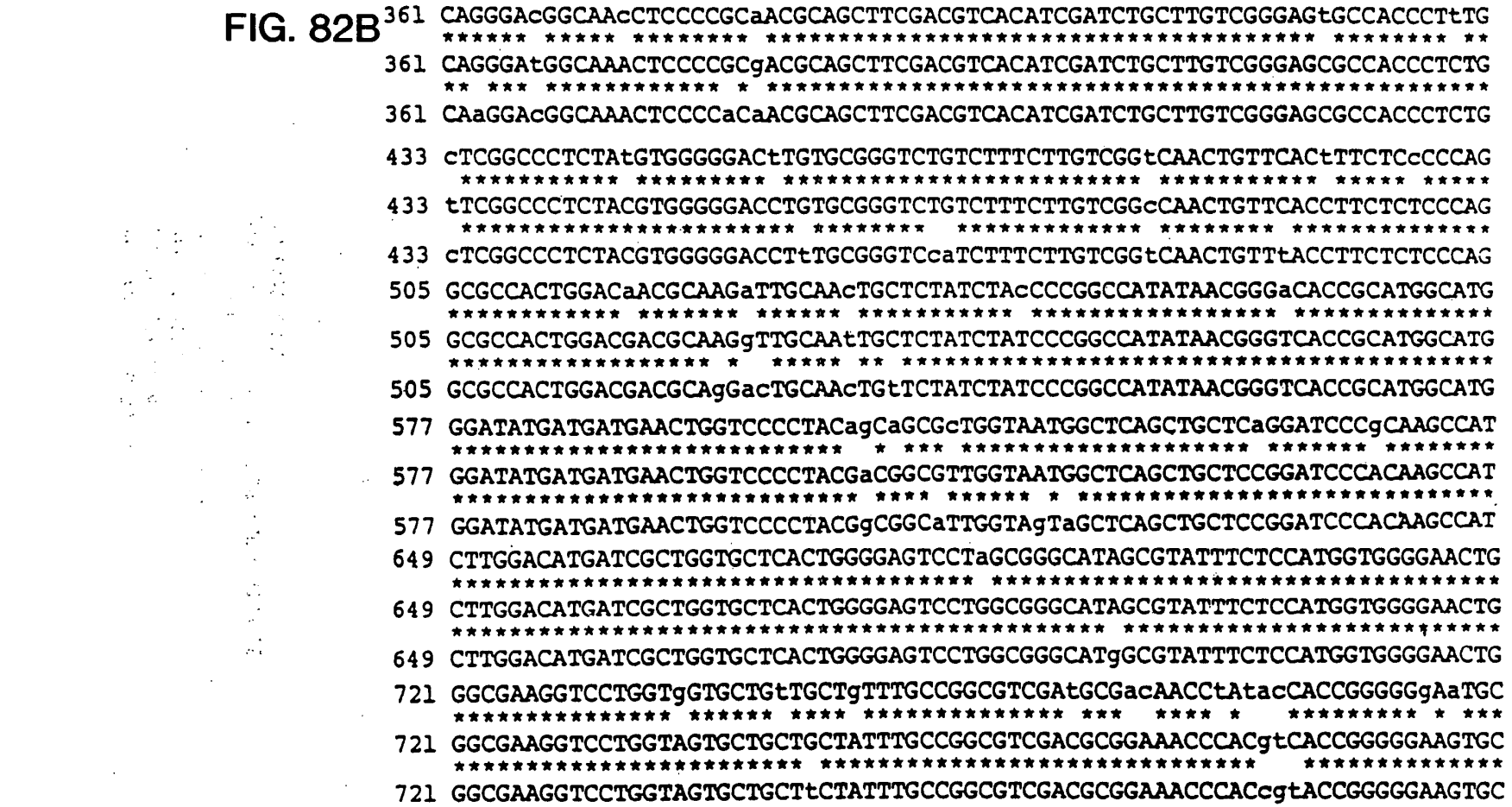


FIG. 82B



```
793 tGcCaggACcacGcagGcgcTcaccAGttTttTCagcCCAGGCGCCAAGCAGgAtaTCCAGCTGATCAACAC
     * *   **   *   *   *    ** *  **   *************** *  ****************
793 CGgCCaCACtgtGtCTGGAtTTGtTAGcCTCcTCgCACCAGGCGCCAAGCAGAACgTCCAGCTGATCAACAC
    ** ** **    * ***** *** *** *** ** ********** * ******* ****************
793 CGcCCgCAgcacGgCTGGAgTTGcTAGtCTCtTCaCACCAGGCGCtAgGCAGAACaTCCAGCTGATCAACAC

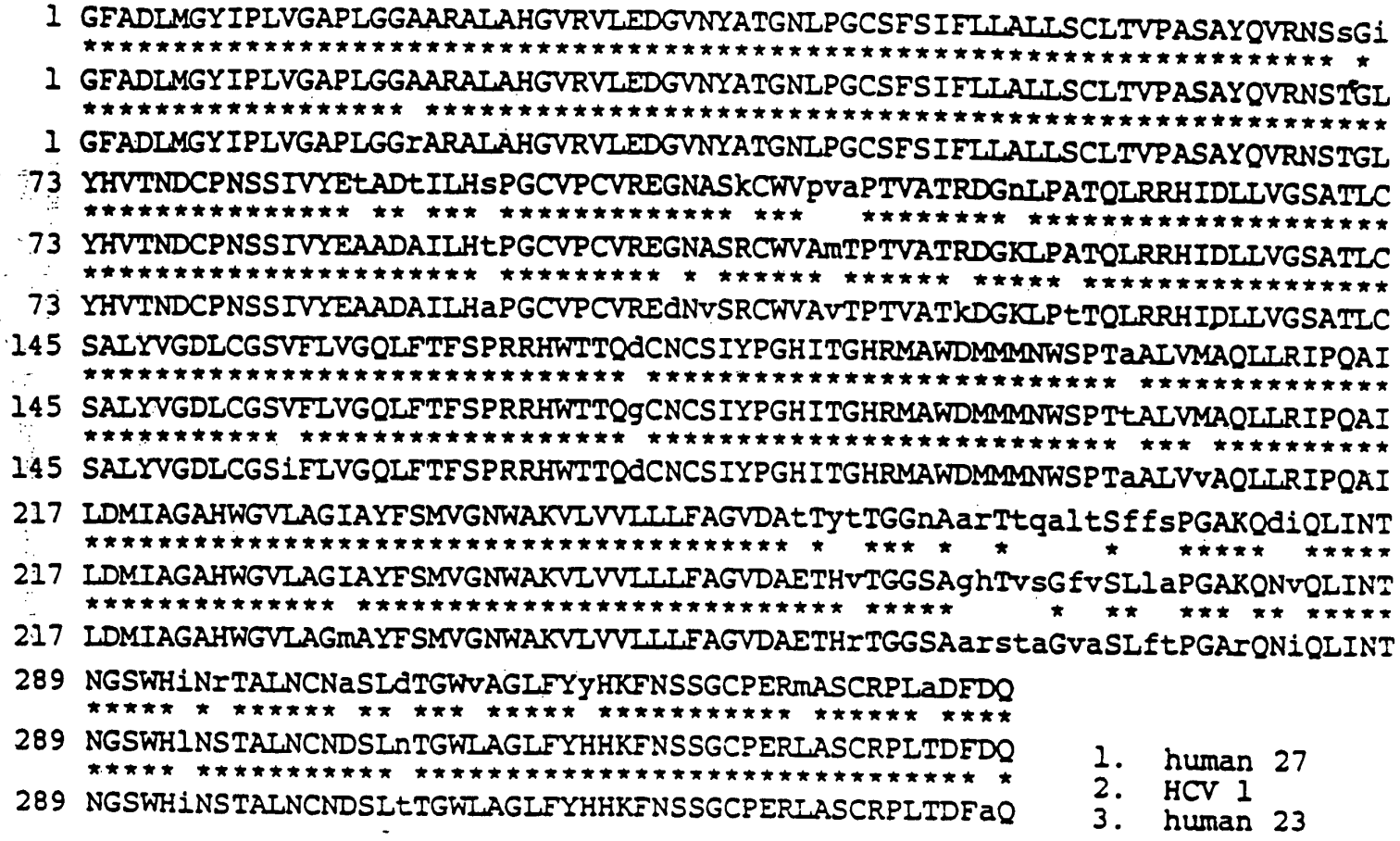
865 CAACGGCAGTTGGCACaTCAATcGCACGGCCtTGAACTGtAATGcgAGCCTCgACACtGGCTGGgTaGCgGG
    **************** ***** ******** ******* ****  ****** **** ****** * ** **
865 CAACGGCAGTTGGCACcTCAATAGCACGGCCcTGAACTGCAATGAtAGCCTCAACACCGGCTGGTTgGCaGG
    **************** ******* ****** ************* ***** * ************ ** **
865 CAACGGCAGTTGGCACaTCAATAGtACGGCCtTGAACTGCAATGAcAGCCTtAcCACCGGCTGGTTaGCgGG

937 GCTcTTCTATtACCACAAaTTCAACTCTTCAGGCTGcCCcGAGAGGaTgGCCAGCTGtaGgCCCCTTgCCGA
    *** ****** ******* ****************** ** ****** * ********  * ****** ****
937 GCTTTTCTATCACCACAAgTTCAACTCTTCAGGCTGTCCtGAGAGGcTaGCCAGCTGCCGACCCCTTACCGA
    *************** ** ******************** ****** * ***************** *****
937 GCTTTTCTATCACCAtAAaTTCAACTCTTCAGGCTGTCCcGAGAGGtTgGCCAGCTGCCGACCCCTcACCGA

1009 TTTcGACCAGG
     *** *******
1009 TTTTGACCAGG
     ***** *****
1009 TTTTGcCCAGG
```

FIG. 82C

FIG. 83



1. human 27
2. HCV 1
3. human 23

FIG. 84

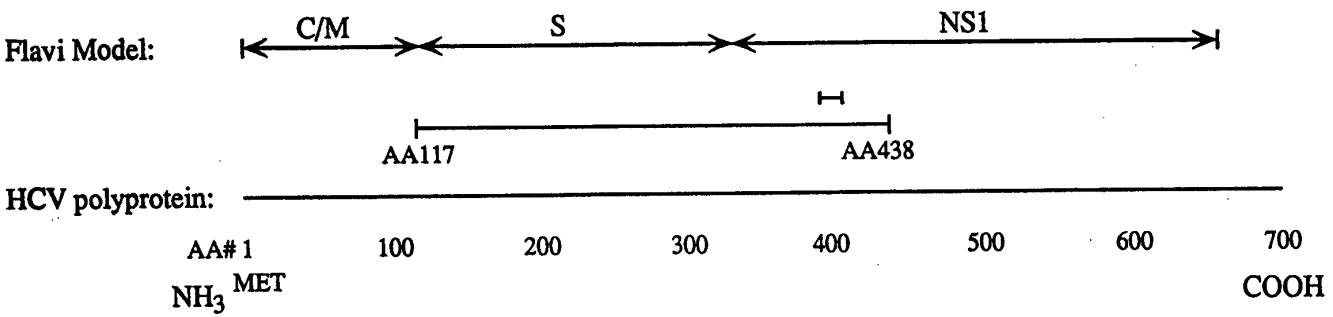


FIG. 85A

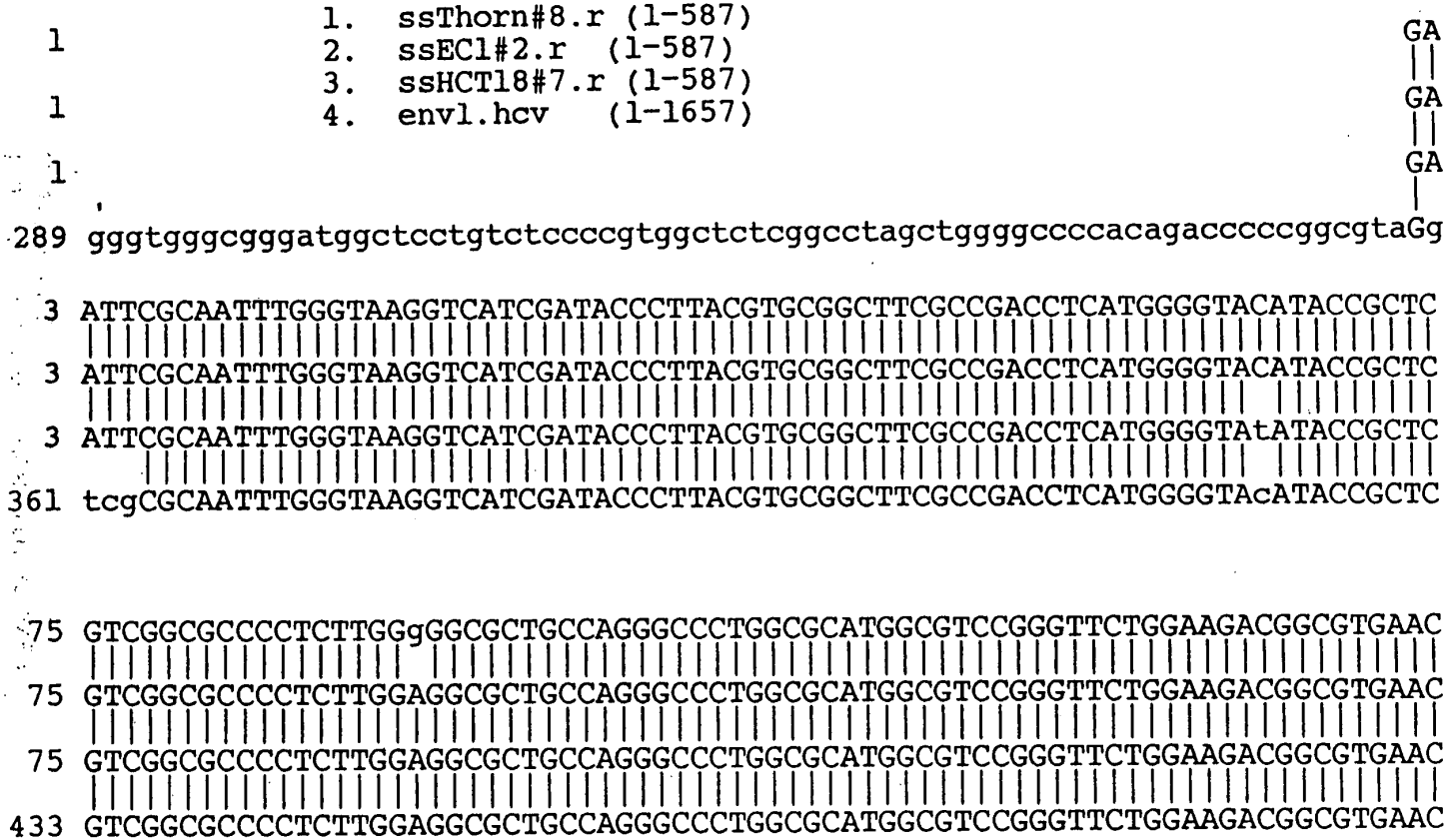
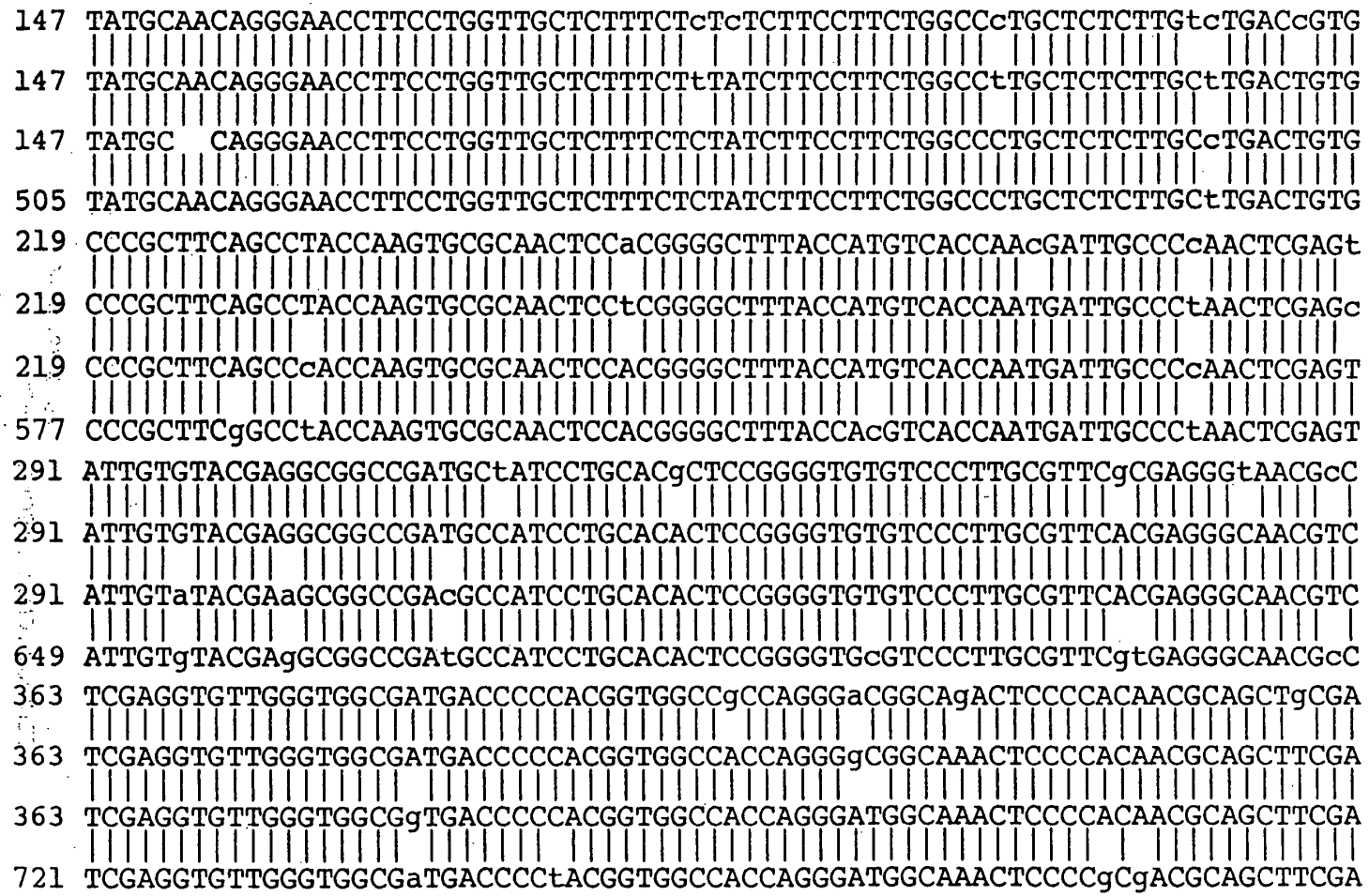


FIG. 85B



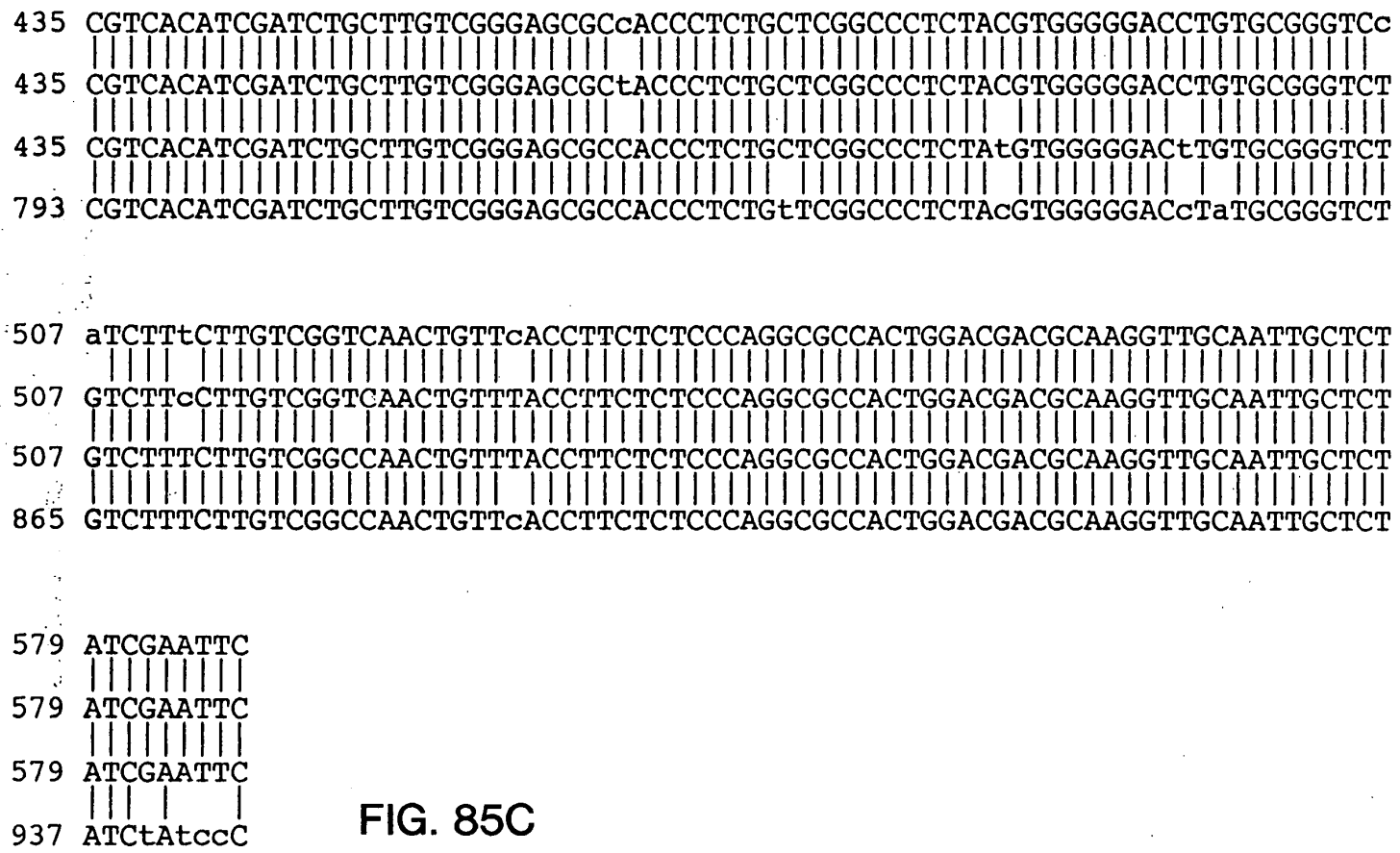


FIG. 85C

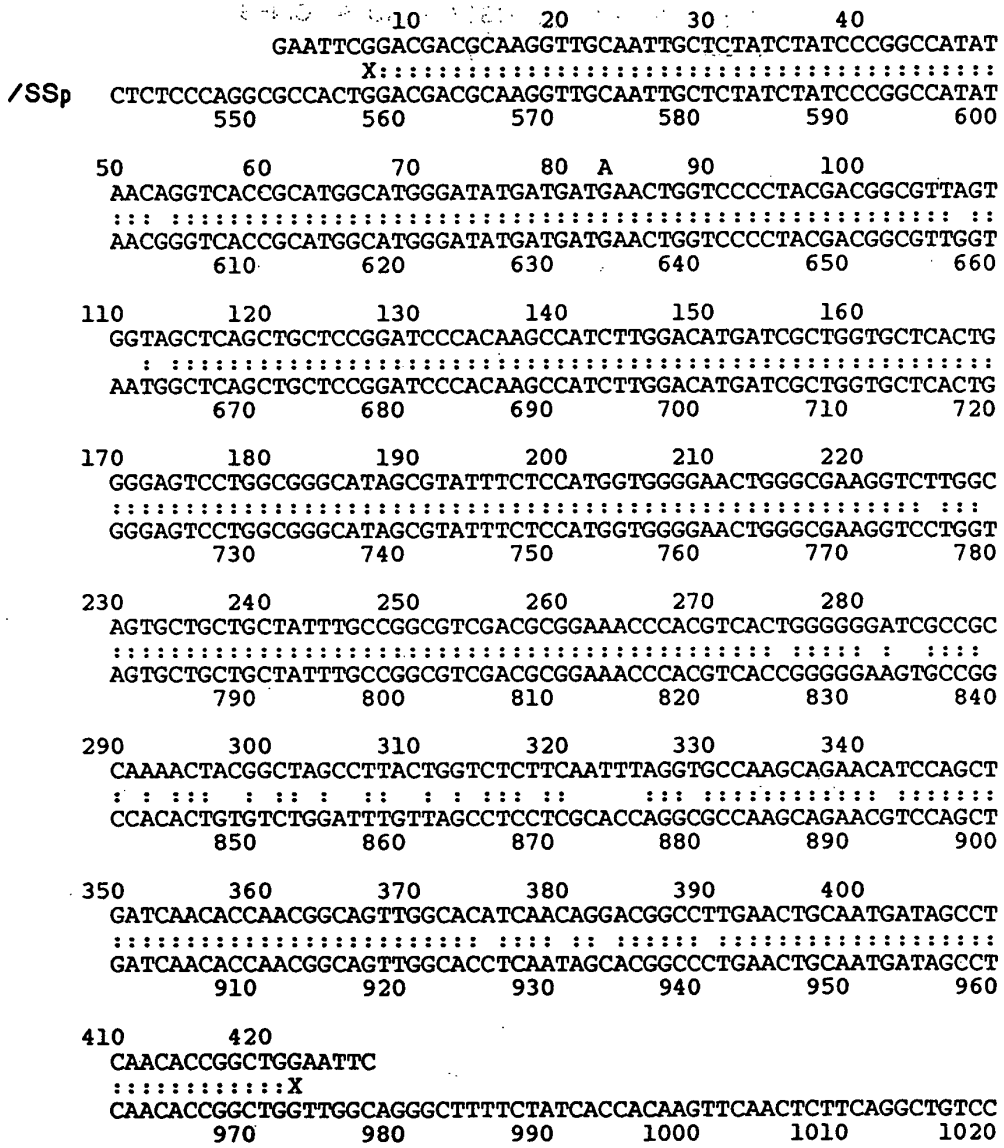


FIG. 86

AA #117-308 (putative envelope region)

FIG. 87

1) HCT #18 (USA) 3 clones sequenced
2) JH23 (USA) ?
3) JH 27 (USA) ?
4) PBL-Th (USA) 2 clones sequenced
5) EC1 (Italy) 3 clones sequenced
6) HCV-1 (chimpanzee) multiple

C/M←→S

1) (P)
2)
3)
4)
5)
6)RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNL

1) H
2)
3) S T T
4) L
5) (F) S
6)PGCSFSIFLLALLSCLTVPASAYQVRNSTGLYHVTNDCPNSSIVYEAADAILH

1) Y (H) V V T
2)A D V V K T
3)S PVA N
4)A A R T
5) H V T
6)TPGCVPCVREGNASRCWVAMTPTVATRDGKLPATQLRRHIDLLVGSATLCS

1)
2) I D
3) D
4)
5) I
6)ALYVGDLCGSVFLVGQLFTFSPRRHWTTQGCNCSI

SUMMARY: "S" AA117-308 (93%)

HCT#18, PBL-Th, EC1(Italy) have 97% homology with HCV-1
JH23 and JH 27 have 96% and 95% homology with HCV-1,respectively

AA#300-438 (C-terminal region of the putative envelope region and amino ~1/3 of NS1)

1) JH23 ?
2) JH27 ?
3) Japanese isolate (T. Miyamura) ?
4) EC10 (Italy) 2 clones sequenced (one nt difference, which did not result in an amino acid change)

5) HCV-1 (chimpanzee) multiple

S ⟷ NS I

1) D A V
2) D A
3) V S VM V
4)
5)TTQGCNCSIYPGHITGHRMAWDMMMNWSPTTALVMAQLLRIPQAILDMIAGA

1) M R A RST A VA
2) T YT N A R TQALT F
3) L Y I M GH R VQ VT TLT
4) A I AK TASLTA
5)HWGVLAGIAYFSMVGNWAKVLVVLLLFAGVDAETHVTGGSAGHTVSGFVSL

1)FS R I I T V
2)FT DI I R A D
3)FR S KI V I R Q F
4)FNL I I R N
5)LAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWL

SUMMARY: NS 1 AA 330-660

"Isolate"	%Homology (AA330-438)	%Homology (AA383-405)
JH23	83	57
JH27	80	39
Japanese	73	48
EC10 (Italy)	84	48

FIG. 88

FIG. 89A

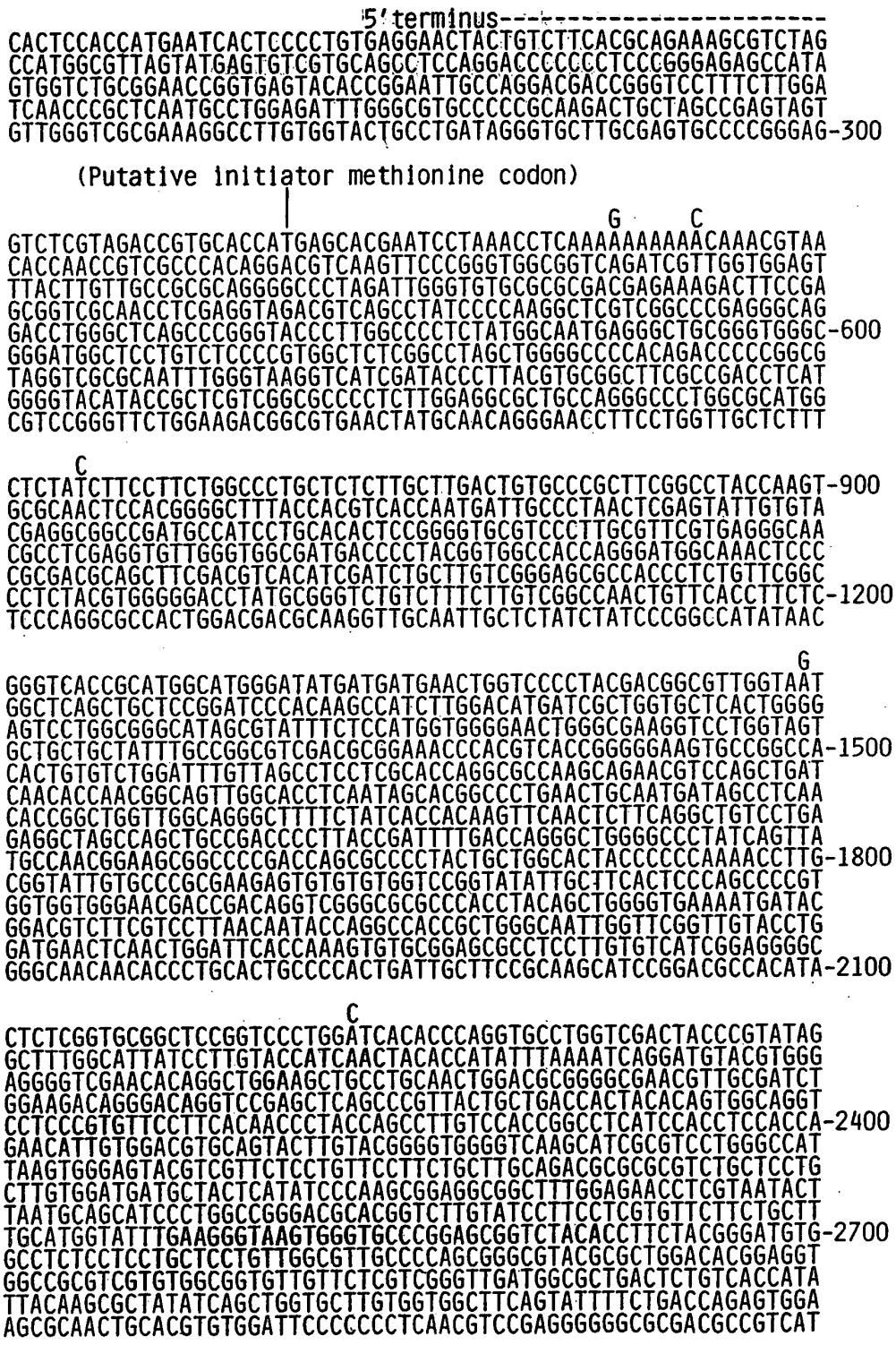


FIG. 89B

```
CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGC-3000
CGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCG
CGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGT
GCAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC
TCCTCTTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGT
CGTCTTCTCCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCGG-3300
TGACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCCGGGAGATACTGCTCGGGCC
AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA
GCAGACAAGGGGCCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA
AGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCCTGGCAACGTGCAT
CAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAA-3600

                                                              T
GGGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCC

         C
GCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCAC
GAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTC
GCCCCGGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGG
GCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGA-3900
CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTC
CTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCCACAGGCAG
CGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT
CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGAT

     T
CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTC-4200
CACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAAT
TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGA
CCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC
CGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC
TTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTG-4500
TCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGC
CGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGT

                                                             A
CGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTG
CAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGAC
AATCACGCTCCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGG-4800
GAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTC
GTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCGCCGA
GACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCA
TCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATC
CCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTG-5100
CGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCT
CAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGA
AATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGA
GGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTG
CCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAAT-5400
CATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCA
CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG
CCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTG
GCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATA
CTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC-5700
AGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGG
GTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTT
AGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGG
GTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCC
CTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGT-6000
CGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCA
GTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTA
CGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAAC
CCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGG
```

FIG. 89C

```
TTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG-6300
GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGG
GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA
GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAA
CATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCC
TGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG-6600
GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG
CCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGC
GCCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATA
CCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCAT
GCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATC-6900
ACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC
TTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG
GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGA
CTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAAT
CCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAA-7200
CCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTG
TCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGT
CCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAG
CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTC
TGGCTGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGA-7500
GCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGC
GGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTG
CGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCA
CAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATT
TGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGC-7800
GGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCC
ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA
GGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAAT
AGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCG
TAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGC-8100
TTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCA
ATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCC
AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG
TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAA
GTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTG-8400
CGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCAC
TTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCT
CGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGC
GAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCC
ACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCA-8700
CGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAG
AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT
GTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTAT
AGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCAT
AGAACCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACT-9000
CCACAGTTACTCTCCAGGTGAAATTAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGT

                    G
ACCGCCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAG
AGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCT
CAAACTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGG
CTACAGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTT-9300
TTGCCTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAAGGTT
GGGGTAAACACTCCGGCCT----------3'terminus
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Some clonal heterogeneities producing amino acid substitutions are shown. There are many other "silent mutations (not shown).

FIG. 90A

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         R T
MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR
KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP-100
RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA

                                  T
LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL-200
YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD
GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT-300

                                        V
TQGCNCSIYPGHITGHRMAWDMMMNWSPTTALVMAQLLRIPQAILDMIAG
AHWGVLAGIAYFSMVGNWAKVLVVLLLFAGVDAETHVTGGSAGHTVSGFV-400
SLLAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWLAGLFYHHKFNSS
GCPERLASCRPLTDFDQGWGPISYANGSGPDQRPYCWHYPPKPCGIVPAK-500
SVCGPVYCFTPSPVVVGTTDRSGAPTYSWGENDTDVFVLNNTRPPLGNWF
GCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPDATYSRCGSG-600

  I
PWLTPRCLVDYPYRLWHYPCTINYTIFKIRMYVGGVEHRLEAACNWTRGE
RCDLEDRDRSELSPLLLTTTQWQVLPCSFTTLPALSTGLIHLHQNIVDVQ-700
YLYGVGSSIASWAIKWEYVVLLFLLLADARVCSCLWMMLLISQAEAALEN
LVILNAASLAGTHGLVSFLVFFCFAWYLKGKWVPGAVYTFYGMWPLLLLL-800

                                                  (N)
LALPQRAYALDTEVAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFL
TRVEAQLHVWIPPLNVRGGRDAVILLMCAVHPTLVFDITKLLLAVFGPLW-900
ILQASLLKVPYFVRVQGLLRFCALARKMIGGHYVQMVIIKLGALTGTYVY
NHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADTAACGDIINGL-1000
PVSARRGREILLGPADGMVSKGWRLLAPITAYAQQTRGLLGCIITSLTGR
DKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQM-1100

             S  T
YTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRG
SLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEN-1200
LETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGSGKSTKVPAAYAAQGYK

                                  L
VLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFL-1300

ADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATAT
PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKC-1400
DELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS

   Y              (S)
VIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYR-1500
FVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPV
CQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLPYLVAYQATVCARAQAP-1600
PPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEITLTHPVTKYIMTCMS
ADLEVVTSTWVLVGGVLAALAAYCLSTGCVVIVGRVVLSGKPAIIPDREV-1700
LYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAV
QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSP-1800
LTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLID
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FIG. 90B

(G)
ILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAA-1900

(HC)
ILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSS
LTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTWLKAKLM-2000

(V)
PQLPGIPFVSCQRGYKGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPR
TCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEEYVEIRQVGDFH-2100
YVTGMTTDNLKCPCQVPSPEFFTELDGVRLHRFAPPCKPLLREEVSFRVG
LHEYPVGSQLPCEPEPDVAVLTSMLTDPSHITAEAAGRRLARGSPPSVAS-2200
SSASQLSAPSLKATCTANHDSPDAELIEANLLWRQEMGGNITRVESENKV
VILDSFDPLVAEEDEREISVPAEILRKSRRFAQALPVWARPDYNPPLVET-2300

(S)
WKKPDYEPPVVHGCPLPPPKSPPVPPPRKKRTVVLTESTLSTALAELATR

(FA)
SFGSSSTSGITGDNTTTSSEPAPSGCPPDSDAESYSSMPPLEGEPGDPDL-2400
SDGSWSTVSSEANAEDVVCCSMSYSWTGALVTPCAAEEQKLPINALSNSL
LRHHNLVYSTTSRSACQRQKKVTFDRLQVLDSHYQDVLKEVKAAASKVKA-2500

(F)
NLLSVEEACSLTPPHSAKSKFGYGAKDVRCHARKAVTHINSVWKDLLEDN
VTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT-2600
KLPLAVMGSSYGFQYSPGQRVEFLVQAWKSKKTPMGFSYDTRCFDSTVTE

(G)
SDIRTEEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCGYRRCR-2700
ASGVLTTSCGNTLTCYIKARAACRAAGLQDCTMLVCGDDLVVICESAGVQ
EDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDGAGKR-2800
VYYLTRDPTTPLARAAWETARHTFVNSWLGNIIMFAPTLWARMILMTHFF
SVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRLHGLSAFSLHSYSPG-2900

G
EINRVAACLRKLGVPPLRAWRHRARSVRARLLARGGRAAICGKYLFNWAV

(P)
RTKLKLTPIAAAGQLDLSGWFTAGYSGGDIYHSVSHARPRWIWFCLLLLA-3000
AGVGIYLLPNRO-3011

Stop codon

( ) = Heterogeneity due possibly to 5' or 3' terminal cloning artefact.

FIG. 91